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Post-processing: Minimum Match 0% Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                   Score
                                                                                               seg length: 10 seg length: 110
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
7: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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10074.554 Million cell updates/sec
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    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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; ANTI-SENSE: US-08-481-658B-65
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76	76	83	83	83	83	83	84	84	84	84	60	60	60	60	78	78	78
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US-08-340-426D-69	US-08-454-557C-69	US-08-787-739-66	US-08-485-862B-66	US-08-486-756A-66	US-08-477-504A-66	US-08-481-658B-66	PCT-US95-17111A-91	US-08-450-673C-91	US-08-340-426D-91	US-08-454-557C-91	PCT-US95-17111A-57	US-08-450-673C-57	US-08-340-426D-57	US-08-454-557C-57	PCT-US95-17111A-70	US-08-450-673C-70	US-08-340-426D-70
Sequence 69, Appl	Sequence 69, Appl	•	Sequence 66, Appl	•	•	Sequence 66, Appl	-	Sequence 91, Appl	-	•	-	•	•		Sequence 70, Appl	Sequence 70, Appl	Sequence 70, Appl

ALIGNMENTS

Sequence 65, Application US/08481658B Patent No. 5955075 GENERAL INFORMATION: APPLICANT: Zavada, Jan APPLICANT: Pastorekova, Silvia APPLICANT: Pastorek, Jaromir TITLE OF INFORTION: MN Gene and Protein NUMBER OF SEQUENCES: 86 CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/260,190 FILING DATE: 15-JUN-1994 ATTORNEY/AGENT INFORMATION: NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863 REFERENCE/DOCKET NUMBER: D-0021.3E TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs STREET: 6 Mariposa Court CITY: Tiburon STATE: California COUNTRY: USA MOLECULE NO HYPOTHETICAL: NO ZIP: 94920 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: TELEPHONE: 415-435-2034 APPLICATION NUMBER: US/O FILING DATE: 07-JUN-1995 CLASSIFICATION: 424 TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear ŏ DNA (genomic) Lauder US/08/481,658B 65: D-0021.3E

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Score 76.8; DB 4; Pred. No. 4e-07;

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; Sequence 65, Application US/08477504A

; Patent No. 5972353
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                24102 CTGGCCAACATGGTGAAACCCCGTCTCTACTAAAATACAAAAAA 24145
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                             24042 ATCCCAGCACTTTGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAAGACCATC 24101
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STREET:
CITY: Tiburon
CITY: California
""ATE: California
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APPLICANT: Pastorekova, Silv.
APPLICANT: Pastorek, Jaromir
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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CTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAA 2
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                                                              ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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                                                                                                                          Score 76.8; DB 4; Length 105; Pred. No. 4e-07; O; Mismatches 17; Indels
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                   Patent No.
                                                                                                                                                      Sequence 65, Application US/08485862B Patent No. 5989838
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                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             24042 ATCCCAGCACTITGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAAGACCATC 24101
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APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAL PC-LOSS #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 424
                            TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
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ANTI-SENSE:
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
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STREET:
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STRANDEDNESS: single
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6 Mariposa Court
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VENTION: MN Gene and Protein
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                                                                                                 Pastorekova, Silvia
                                                                                                                   Zavada, Jan
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                                                                                     Jaromir
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Pred. No. 4e-07;
0; Mismatches 17;
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; ANTI-SENSE: NO
US-08-485-862B-65
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                                                                                                                                                                                                                                                                                                                Patent No. 6027887
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       Sequence 65, Application US/08787739 Patent No. 6027887
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Best Local S
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TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24102 CTGGCCAACATGGTGAAACCCCGTCTCTACTAAAATACAAAAA 24145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24042 ATCCCAGCACTTTGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAAGACCATC 24101
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                  APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DN
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                               45 CTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/477,504 FILING DATE: 07-JUN-1995 APPLICATION NUMBER: US 08/260,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                    94104
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US-08-481-658B-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-981-0332 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                   24102 CTGGCCAACATGGTGAAACCCCGTCTCTACTAAAATACAAAAAA 24145
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APPLICATION NUMBER: US 01
FILING DATE: 07-JUN-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                    TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
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HYPOTHETICAL:
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COMPUTER READABLE FORM:
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                                    STREET: 6 Maripose
CITY: Tiburon
STATE: California
                COUNTRY:
ZIP: 949
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                                                                                                                                                                                                                                                                                                                  45 CTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAA 2
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STRANDEDNESS: double
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                                                                                           ADDRESSEE:
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                94920
                                                                                                                                                                                                                      5, Application US/08481658B
5955075
                                                                      6 Mariposa Court
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Pred. No. 4e-07;
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ches 17; Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:

MEDIUM TYPE: Flopp COMPUTER: IBM PC c OPERATING SYSTEM: SOFTWARE: Patentin

PC compatible EM: PC-DOS/MS-DOS

Floppy disk

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16770 TGCCCTCAAGTGATCCTCCTGCCTCGGCCTCCCAATGTGCTGGGAT 16815
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INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 86
CORRESPONDENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
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APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: TORNEY TORNEY
                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                           CITY: Tiburon
STATE: California
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                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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                                                                                                                                                                                                                                                          COUNTRY:
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85.8%;
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                                                                                                         US/08/477,504A
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Pred. No. 5.4e-06;
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US-08-486-756A-65; Sequence 65, Application US/08486756A; Patent No. 5981711
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                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDITIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION UMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Landar Leona I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
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                                                                    TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                      REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                         NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
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STRANDEDNESS: sing
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CITY: Tiburon
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 STRANDEDNESS:
                     TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
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                nucleic acid
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                                                                                        415-435-0727
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single
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Pred. No. 5.4e-06;
0; Mismatches 13
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; ANTI-SENSE: 1
US-08-486-756A-65
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                                                                                                    ; ANTI-SENSE: US-08-485-862B-65
Query Match
Best Local Similarity 85.0
Conservative
                                                                                                                                                                                                                                          FILING DATE: 15-JUN-1994
ATTORNEY_AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
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Patent No. 5
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Best Local Similarity
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LENGTH: 105 base pairs
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/485,862B FILING DATE: 07-JUN-1995
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                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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cal Similarity 85.8%;
91; Conservative
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                                                                                                                                               DNA (genomic)
                                  0.2%; Score 71.2; DB 4; 85.8%; Pred. No. 5.4e-06;
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Pred. No. 5.4e-06;
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                       Mismatches
                                                   DB 4; Length 105;
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APPLICANT:
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APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER: US 01
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
ETLING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ANTI-SENSE:
                            MOLECULE TYPE:
                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
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ATTORNEY/AGENT INFORMATION:
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                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                        TELEPHONE: 415-981-20
TELEFAX: 415-981-0332
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US OF STRING DATE: 07-JUN-1995
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                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                    NAME: Lauder, Leona L. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
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STATE: California
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                                                         TOPOLOGY:
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                                                                                            nucleic acid
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369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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NO
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                  NO
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                                   DNA (genomic)
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US-08-454-557C-91/c
; Sequence 91, Application US/08454557C
; Patent No. 5830670
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US-08-340-426D-91/c
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
Sequence 91, Application US/08340426D Patent No. 5948634
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Best Local Similarity
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Best Local 9
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                                                                                                                                    24092 CAAGACCATCCTGGCCAACATGG 24114
                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
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APPLICANT: Wands, Jack R.
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ATTORNEY/AGENT INFORMATION:
                                                                                                    23 CGACACCAGCCTGATGAACATGG
                                                                                                                                                                       Local Similarity
nes 72; Conserv
                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
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86.7%;
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Pred. No. 5.4e-06;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Index: Structure
Index: Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.2%;
Best Local Similarity 86.7%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                    Sequence 91, Applicat Patent No. 5948888 GENERAL INFORMATION:
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APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Florer
COMPUTER
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                        TITLE OF INTERPOLES: 121

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

ADDRESSEE: Sterne, Kessler, Suite 600
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                               APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R.
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LENGTH: 84 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                       STATE:
                                                                                                                                                    STREET: 1100 New CITY: Washington
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PatentIn Release #1.0,
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Pred. No. 7.4e-05;
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  Version
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION:

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Sequence 91, Application PC/TUS9517111A

Sequence 91, Application PC/TUS9517111A

GENERAL INFORMATION PC/TUS9517111A

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and

TITLE OF INVENTION: Detection of Alzheimer's Disease
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Best Local Similarity 86.7%;
Matches 72; Conservative (
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILLING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/1711:
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NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
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                                                                                     NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C STREET: 1100 New York Avenue, Suite 600
                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 20005-3934
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STRANDEDNESS
                                    ENGTH:
                  nucleic acid
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Pred. No. 7.4e-05;
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RESULT 15
US-08-454-557C-70
US-08-454-557C-70
; Sequence 70, Applicatic
; Patent No. 5830670
; GENERAL IMFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
LENGTH: 78 base pairs
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Best Local Similarity
Matches 72; Conserv
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Best Local Similarity
Matches 67; Conserv
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                                   9546 CTGGTGTTGAACTCCTGA 9563
                                                                                                               9486 ACCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGG 9545
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: de la Monte, 9
APPLICANT: Wands, Jack R.
61
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                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 20005-3934
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CTGGTGTCGAACTCCTGA 78
                                                                          ACAACGCCCAGCTAATATTTGTATTTTAGTAGAGATGGGGTTTCTCCATGTTCATCAGG 60
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86.7%;
                                                                                                                                                    0.2%; Score 60.4; DB 3;
85.9%; Pred. No. 0.00074;
ative 0; Mismatches 11;
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Search completed: June 16, 2000, 20:15:34 Job time: 199264 sec

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Title:
Perfect score:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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GenEmbl: *
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-968.237 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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9b_p12:

9b_pr2:

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45: gb_htg7:*
46: em_htg2:*
47: em_htg2:*
48: em_htg3:*
49: em_hmm5:*
50: gb_p13:*
51: gb_pr5:*
52: gb_htg9:*
53: gb_htg10:*
54: gb_htg10:*
55: gb_htg11:*
56: gb_htg12:*
57: gb_htg13:*
58: gb_htg13:*
58: gb_htg14:*
Pred. NO. 1s the number of results predicted by chance
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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SOURCE
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KEYWORDS
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HSLDLRN2
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                                                                                                                                         Eur. J.
87161901
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                                                                                                                                                      Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
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Alu repetitive sequence; low density lipoprotein receptor.
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke,B., Beisiegel,U., Dunning,A., Havinga,J.R.,
Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences the low-density-lipoprotein-receptor gene. A possible mechanism
                                                                                                                                                                                                                                                                                                                                                                          91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alu RNA transcripts in human embryonal post-transcriptional selection of masta J. Mol. Biol. (1992) In press
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Sinnett, D., Richer, C., Deragon, J.-M. and Labada, D.
                                                                                                                                               X05249.1
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Alu repeat.
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
                                                                                                                                               GI:34335
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="carcinoma"
30 c 35 g 1
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Alu RNA transcript, clone CE162.
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia European School (1), 77-81 (1987)
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See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion occurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
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In the defective LDL-receptor gene the deletion occurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
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1 (bases 1 to 108)
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
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Unequal crossing-over between two alu-repetitive DNA sequences i the low-density-lipoprotein-receptor gene. A possible mechanism the defect in a patient with familial hypercholesterolaemia the defect in Beisen, J. Blochem. 164 (1), 77-81 (1987)
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In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
                                                 Homo sapiens
                                                                             Alu repetitive
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                                                                                                                                          HSLDLRD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES
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Alu repetitive sequence; low density lipoprotein receptor.
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                                                                                               GI:34336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="blood leukocytes from a patient with familial"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur., J. Blochem. 164 (1), 77-81 (1987)
                                                                90;
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells.
post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES
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                                                                                                                                                          /tissue_type="carcinoma"
27 c 33 g 1
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/cell_type="blood leukocytes
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/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P Direct Submission
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1 (bases 1 to 108)
                                                   Shaikh, T.H., Roy, A.M., Kim, J., cDNAs derived from primary and
                                                                           Eutheria; Primates; Catarrhini; Hominidae;
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/rpt_type=dispersed
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/db_xref="taxon:9606"
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Submitted (22-AUG-1996) Human Genetics and Molecular Biology, Children's Hospital of Philadelphia, 1004F Abramson Research Children's Hospital of Philadelphia, Philadelphia, PA 19104, U
                                             87;
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X57789
X57789.1 GI:23938
X57789.1 gi:23938
                                                                                                                                                                                                                                                                           Nucleic Acids Res. 19 (17), 4787 (1991) 91367697
                                                                                                                                                                                                                                                                                                                  Butler,R., Riley,J.H., Ogilvie,D.J., Anand,R., Buxton,J., Davies,J., Johnson,K. and Markham,A.F.
Two sequence-tagged sites defining the ends of a 380 kb Y
                                                                                                                                                                                                                                                                                                                                                           Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals, Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK 2. (bases 1 to 103)
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/db_xref="taxon:9606"
/chromosome="19q13"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
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J. Mol. Biol. (1992) In press
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
                                                                                                                                        post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/cell_line="NTera2D1"
/tissue_type="carcinoma"
27 c 33 g 1
                             /dev_stage="embryo"
/sex="male"
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/sex="male"
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Submitted (22-AUG-1996) Human Genetics and Molecular Biology,
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, U
 Alu
                            density lipoprotein.
X05248
                                                     Human LDL-receptor gene intron 12 fragment (normal gene) LDL =
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Shaikh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 110)
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repetitive sequence;
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/rpt_family="Alu"
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/db_xref="taxon:9606"
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1 (bases 1 to 108)

Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,

Williamson, R. and Humphries, S.

Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism the defect in a patient with familial hypercholesterolaemia Bur. J. Biochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                       see X05249 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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/note="Alu repeat"
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Matches

84;

Conservative

0.2%; Score 72; DB 1; Length 108; 79.2%; Pred. No. 0.011; rative 1; Mismatches 21; Indels

21; Indels

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Gaps

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8545 CAAGTGATCTGCCCACCTTGGCCCCTCCATAGTGCTGGGATTACAG 8590

CAAGTGATCCGTCTGCCTTGGCCTCCCAAAAGTGCTGGGATTATAG 108

Query Match Best Local Similarity

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                                                                                         cell typing; a Homo sapiens. WO9514772-Al.
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X10269-X12937 are human DNA fragments which contain biallelic
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Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Human biallelic, human; forensic; paternity testing; disease; Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                             1199
                                01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                               07-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-1997; U20313.
06-NOV-1996; US-030455.
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                                                                                                                                                                                                                                                                                                                                                                      AGACCAGCCTGACCAACATGGCAAAAACCTCATCTCTACTAAAAATACA 1246
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                                                                                                                                                                                                                                                                                                                                                  AGACCATCCTGGCCAACAYAGGAAAACCTCATCTCTACAAAAAAGACA 1
                                                                                                                                                                                         V-1996 (first entry)
gene signature HUMGS07131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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BP;
                                                                                                                                                                                                                                                    cDNA to
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                                                                                                                                                                                                                                                    mRNA;
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Pred. No. 0.022;
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                                                                                                                                                                     relative abundance; frequency;
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A single-stranded DNA (or its complementary strand or the corresp.

C double-stranded DNA) which comprises one of the 7837 "GS" sequences

C double-stranded DNA) which comprises one of the 7837 "GS" sequences

C given in T19001-T26837 and which is able to hybridise to part of

C human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

C sequences were obtained from 3'-directed cDNA libraries prepared

C from various human tissues; synthesis of cDNA was initiated from the

3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

C untranslated sequence is unique to a particular mRNA species, almost

C all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

C is constructed so as to reflect accurately the relative abundance of

C different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

C determined (esp. using primers and probes derived from the GS

c sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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                Claim 1; Page 1720; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                 Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                tissues
                                                                                                                                                                                                                                                                                                                                              Matsubara K, Okubo K;
WPI; 95-206931/27.
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12-NOV-1993;
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WO9514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                        (MATS/) MATSUBARA K.
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  The appearance frequency
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108 BP; 34 A; 31 C;
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JP-355504.
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Pred. No. 0.05;
given GS
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RESULT
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                                                                                   Pri detecting nucleic acids, telomerase activity, oncogene mutations, or processor aspecific sequences, for diagnosis of disease PS Example 11; Page 318; 478pp; English.

CC A process has been developed for determining the sequence of a target concelled acid. The process comprises: (i) generating at least two cc fragments (F) from the target nucleic acid; and (ii) analysing F by cc mass spectrometry (MS). The sequences in v39483 to v39592 are cc specifically claimed primers for use in the mass spectrometric analysis co f the above process. The process is used to detect genetic diseases cc (e.g. haemophilia, thalassemia, Duchenne muscular dystrophy. Alzheimer's cc disease, cystic fibrosis and many others) or chromosomal abnormalities compared the process and cancers; also for establishing cc dentity and heredity. Particular applications are diagnosis of neuroblastoma, detecting telomerase, determining family relationships and HAA comparibility, and in genetic fingerprinting. Compared with known methods using MS, this process requires fewer specific reagents cand is better suited to automation. Extended primers are shorter; and is better suited to automation. Extended primers are shorter; compared with the process simultaneously. The present sequence represent an cc oligonucleotide used in an example from the present invention.
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Best Local S
Matches 77
Query Match 0.3
Best Local Similarity 98.9
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY 1998.

06-NOV-1997; US-947801.

08-OCT-1997; US-74481.

06-NOV-1996; US-744590.

06-NOV-1996; US-746036.

06-NOV-1996; US-746036.

06-NOV-1996; US-746036.

23-JAN-1997; US-78638.

23-JAN-1997; US-78639.

19-SEP-1997; US-933792.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27660
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Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing nucleic acid by mass spectrometric analysis detecting nucleic acids, telomerase activity, oncogene
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Koster H, Little DP, Lough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsatellite analysis antisense strand SEQ ID NO:262.
Mass spectrometry; diagnosis; detection; biological sample; infection; genetic disease; chromosomal abnormality; identification; heredity; pathogenic organism; telomerase activity; oncogene mutation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer-specific sequence; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SEQU-) SEQUENOM INC.
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Pred. No. 0.09
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 Score 63.4; D
Pred. No. 0.2;
0; Mismatches
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RESULT
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AC T3
AC T3
DT 11
DE Ht
KW GG
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Cdouble-stranded DNA (or its complementary strand or the corresp.

Cdouble-stranded DNA) which comprises one of the 7837 "GS" sequences

Cgiven in T19001-T26837 and which is able to hybridise to part of

CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

CC sequences were obtained from 3'-directed cDNA libraries prepared

CC from various human tissues; synthesis of cDNA was inlitiated from the

CC untranslated sequence is unique to a particular mRNA, secies, almost

CC untranslated sequence is unique to a particular mRNA. Each library

CC is constructed so as to reflect accurately the relative abundance of

CC different mRNAs in the particular tissue from which it was derived.

CC The appearance frequency of a given GS in a cDNA library can be

CC determined (esp. using primers and probes derived from the GS

CC sequences) as a means of diagnosing abnormal cell function or for

CC recognising different cell types.

SQ Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                  22621 TTTATTTTTTTGAGACAGAGTCTCACTCTGTCACCCCAGGGTAGAATGCGGTGGTGTGATC 22680
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WO9514772-A1.
01-JUN-1995.
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Human gene signature HUMG$08452. Relative abundance; Gene signature; messenger RNA; relative abundance; human; cloning; mapping; non-blased library; diagnosis; d cell typing; abnormal cell function; ss.
                                                                     T26213;
13-NOV-1996
                                                                                                         T26213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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WPI; 95-206931/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T24892
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12-NOV-1993; JP-355504.
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                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                        standard; cDNA to mRNA;
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                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                     Score 62.4;
Pred. No. 0
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                    detection;
                                  frequency;
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sapiens

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RESULT
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Claim 1; Page 2029; 2245pp; Japanese.

Claim 1; Page 2029; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

Clouble-stranded DNA, which comprises one of the 7837 "GS" sequences

Clouble-stranded DNA, which comprises one of the 7837 "GS" sequences

Clouble-stranded DNA, which is able to hybridise to part of

Chund 1 179001-726837 and which is able to hybridise to part of

Chund Genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

Clouble-stranded from 3'-directed cDNA libraries prepared

Clouble-stranded from the sole primer. Since the 3'-

Clountranslated sequence is unique to a particular mRNA species, almost

Clouble-stranded CDNAs hybridise with specific mRNAs. Each library

Clouble-stranded So as to reflect accurately the relative abundance of

Clifferent mRNAs in the particular tissue from which it was derived.

Clouble-stranded (esp. using primers and probes derived from the GS

Cleven Sequences of diagnosing abnormal cell function or for

Clouble-stranded Cell types.

So Sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
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Best Local S
Matches 77
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Claim 1; Page 1748; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared
                                                                                                                                                                                                                                                                                                                                                      Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                             Human
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                 Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                               T25009 standard;
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WPI; 95-2069
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                                                                                                                                                                                                                                                                                                                   Homo sapiens.
WO9514772-A1.
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                                                                                                                                                                                                                           11-NOV-1994; J01916.
12-NOV-1993; JP-355504
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ОКИВ/) ОКИВО К.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                           95-206931/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGACTTGAGCTCCGGAGGGGGAGGTTGCAGTGAGCCCAGATTACACCACTGCACTCCAG 1372
                                                                                                                                                                                                                                                                                                                                                                                                             gene signature HUMGS07131.
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77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               to mRNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 103;
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15085 TGCCTGGCTAATTTTTGTATTATTAGTAGAGATGGGGGTTTCGCCATGTTGGCCAGGCTGG 15144

Query Match Best Local S Matches 70

Similarity

0.2%;

Score 61.6; D Pred. No. 0.37 0; Mismatches

.37; DB 16;

1.

Length

Indels

0

Gaps

0

Conservative

0;

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RESULT
T21566/c
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PS Claim 1; Page 914; 2245pp; Japanese.

Claim 1; Page 914; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. Codouble-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of the man genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA ilbraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

So Sequence 87 BP; 35 A; 21 C; 16 G; 13 T;
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Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27600 ATCACTTGAACTCAGGAGGCAGAGGTTGTAGTGAGCTGAGATCGCACCACCTGCACTCCAG 27659
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T21566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                 Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA th reflects relative abundance of corresp. mRNA in specific human cells.
                                                                                                                                                                                                                                                                                                                                                                                                                           Matsubara K, Okub
WPI; 95-206931/27.
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11-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from various human tissues; synthesis of cDNA was initiated
                                                                                                                                                                                                                                                                                                                                                  tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (окив/) окиво
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; J01916.
; JP-355504.
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73.6%;
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
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                                                                                                                                                                                                                                                                                                                                                                     specific human
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98

TTCTTGGCTNATTTCTGTATTTTTTGTAAAGATGGGGTTTCGCCATGTTCCTCGGGCTGG

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RESULT 11
T26828/c
ID T26828 standard; c
AC T26828;
DT 14-NOV-1996 (firs
DE Human gene signature; me
KW Gene signature; me
KW human; cloning; ma
KW cell typing; abnor
OS Homo sapiens.
PN W09514772-Al.
PD 01-JUN-1995.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                       15145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 758-759; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNAs pecies, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a CNNA library can be
                  Human gene signature HUMGS09078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo sapiens.

W09514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recognising different cell types. Sequence 103 BP; 22 A; 27 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 95-206931/27.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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                                                                                                                                                                                                                                                                                                                                                                                          0.2%;
nilarity 75.8%;
Conservative
                                                                                                                           (first entry)
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                                                                                                                                                              mRNA;
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Pred. No. 0.35
0; Mismatches
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So sequence 108 BP; 18 A; 33 C; 23 G; 28 T;
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Best Local
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Claim 1; Page 1944; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost
                                                                                                                                                                                                                                                                                                                             01-JUN-1995.
11-NOV-1994;
12-NOV-1993;
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                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection;
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WPI; 95-206931/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                  cell typing;
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WPI; 95-206931/27.
                                                                                                                                                                              tissues
                                                                                                                                                                                                                                                                                                          (MATS/) MATSUBARA K.
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12-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene signature HUMGS08084.
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Pred. No. 0.
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 91 BP; 18 A; 22 C; 28 G; 18 T;
                                                                                                                                                                                                                                                3'-end of mrNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mrNA species, almost all the 3'-oriented cDNAs hybridise with specific mrNAs. Each library is constructed so as to reflect accurately the relative abundance of different mrNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be
                                                                                                                                                                                                                                                                                                                                                 A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                               determined (esp. using primers and probes derived sequences) as a means of diagnosing abnormal cell recognising different cell types.

Sequence 108 BP; 18 A; 33 C; 23 G; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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                                                                                                   Local Similarity
nes 76; Conser
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GAGCCACCGTGCCCAGCCTCTTTTTCTTTTCTTATAAGACAAG
                                 95-206931/27.
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                                                                                                 Score 61; DB Pred. No. 0.46 0; Mismatches
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Pred. No. 0.46;
0; Mismatches
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detection;
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RESULT 1
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A single-stranded DNA (or its complementary strand or the corresp. Codouble-stranded DNA), which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) Sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 93 BP; 22 A; 23 C; 24 G; 22 T;
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Best Local S
Matches 72
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                                                             cell typing; a
Homo sapiens.
W09514772-A1.
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11-NOV-1994; J01916.
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                            01-JUN-1995.
11-NOV-1994;
                                                                                            human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                          Gene signature; messenger RNA; mRNA;
                                                                                                                                         Human gene signature HUMGS08452.
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WPI; 95-206931/27.
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W09514772-A1.
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(MATS/)
                12-NOV-1993;
                                                                                                                                                                                           26213 standard;
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JP-355504.
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Pred. No. 0.
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Search completed: June 17, 2000, 11:43:03 Job time: 254694 sec
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Claim 1; Page 2029; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp.

CC double-stranded DNA) which comprises one of the 7837 "GS" sequences

CC given in T19001-T26837 and which is able to hybridise to part of

CC human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature)

CC sequences were obtained from 3'-directed cDNA libraries prepared

CC from various human tissues; synthesis of cDNA was initiated from the

CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

CC untranslated sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

CC is constructed so as to reflect accurately the relative abundance of

CC different mRNAs in the particular tissue from which it was derived.

CC The appearance frequency of a given GS in a cDNA library can be

CC determined (esp. using primers and probes derived from the GS

CC sequences) as a means of diagnosing abnormal cell function or for

CC crecognising different cell types.

SQ Sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                   19110 ACATGGCTCACTGCAGCCTCAACCTACTGAGCTCAAGCAATC 19151
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WPI; 95-206931/27.
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1 TGTTTAGAGGAAAAAAAGCA.....TAGATAAAACGTTGTTCCTT
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Copyright (c) 1993 - 2000
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For BAC

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                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 105)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
         Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                      Homo
                                                                                                                                                           AQ282107 105 bp
RPCI11-94B21.TJ RPCI-11
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Institute for Genomic Research Medical Center Dr., Rockville,
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AA1991750 wt48e01.x
H11143 ym90c06.r1
AA244245 nc07a04.s
AA250812 zs06a05.s
AA565533 nt42b11.3
AQ2635244 RPCI-11-3
AQ263264 CIT-HSP-2
AA244245 nc07a04.s
AA664562 nt75f10.s
AA664562 nt75f10.s
AA664562 nt75f10.r1
AQ386882 RPCI11-13
AQ062963 CIT-HSP-2
AA244209 zr25h02.s
AA835205 ak64h01.s
AQ283340 RPCI11-80
AA129957 zn86h04.r
AI249096 qh73g09.x
AQ386882 RPCI11-13
AQ386882 RPCI11-13
AQ286340 RPCI11-13
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B65160 CIT-HSP-201
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                                                                                                                                                                                        AUTHORS
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                                                                                                 Unpublished (1997)
Other_GSSs: CITHSP-2017G2.TFB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                B65160 108 bp DNA
CIT-HSP-2017G2 TRB CIT-HSP
                                                                                                                                                                                                                                                                                                                                                                                                                 95;
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Clones are derived from the human BAC library RPCI-11. For BA
Clones are derived from the human BAC library RPCI-11. For BA
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or
Research Genetics (lifo@resgen.com). BAC end search page:
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H. Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                               genomic survey sequence.
B65160
                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: M13 Reverse Class: BAC ends.
                                                                       9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301 838 0200 Fax: 301 838 0208
                                              Clones are available end search page:
                                                                                                                                                   Building
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/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
/note="BAC Library"
1 31 c 30 g 18 t
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/db_xref="GDB:7535756"
/db_xref="taxon:9606"
/clone="RPCI-11-94B21"
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                                                        Research Genetics (info@resgen.com). BAC
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Sequence-Ready Map

Shizuya, H.,

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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Other_GSSs: 345K02.TP 345K02.TPB
Contact: Mark Adams
                                                                                                                                                                                                                                                              end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109)

Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
27 c 34 g 21 t
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/db_xref="taxon:9606"
/clone="A-345K02"
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/clone="2017G2"
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/db_xref="GDB:7043860"
                                                                                            /cell_type="Fibroblast"
/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
Calfech Human BAC Library Al"
30 c 31 g 24 t
                                                                                                                                                            /sex="Female"
                                                                                                                                                                          /clone_lib="CIT978SKA1"
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                Score 87.2; DB 84; Pred. No. 0.33;
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                                                                                                                                    22425 GTTCACTGCAACCTCCACCTCCTGGGTTCAAGCGAGTCTCCTGACTCA 22472
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AA703692 106 bp mRNA EST 24-DEC-1997 ag81a10.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1140858 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                     95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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CIT-HSP-2313G15.TF CIT-HSP
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pBeloBAC11; Site_1:
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/db_xref="taxon:9606"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109)
1 (bases 1, Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Hillier,L., Lennon,G., Bubuque,T., Favello,A., Gish,W.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Chiapelli,B.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
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yw52c09.s1 Weizmann Olfactory Epithelium
IMAGE:255856 3' similar to contains Alu z
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High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos: Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)
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Fax: 314 286 1810
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/db_xref="taxon:9606"
/clone="IMAGE:1140858"
/clone=11b="Stratagene hNT neuron (#937233)"
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Pred. No. 0.37;
0; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16961 TGCATTCCAGCCTGGGAGACAGAGCGAGACTCCGTCTCAAAATTAAAAA 17009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCACTCCAGCCTGGGAGACAGAGCGAAGNTCCGTCTCAAAANNAAAAA
                                                                                                                                                                                                                                                                                                                 107 bp mRNA EST99495 Thyroid Homo sapiens Alu repeat, mRNA sequenca AA385808
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 107)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97044478
On Apr 14, 1993 this sequence version replaced
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                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="olfactory epithelium"
/dev_stage="35 year old"
/lab_host="SOIR cells (kanamycin resistant)"
/note="organ: nose; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Olfactory epithelium, normal. Average insert
size: 0.8 kb; Uni-ZAP XR Vector. Library constructed by Nalker, D. Lancet, Weizmann Institute of Science. -5'
walker, D. Lancet, Weizmann Institute of Science. -5'
adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
sequence: 5' CTCGACTTTTTTTTTTTTTTTTT 3'"
a 34 c 24 g 35 t 3 others
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/db_xref="GDB:3866265"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:255856"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCGCCACTGCACCTCGACCTGGGTNACAGAGCGAGACTCTGTCTC 1
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                                                                                                                                                                                                                                                                                                                                   AASU3697 101 bp mRNA EST 26-SEP-1997 nn58f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1088107 similar to contains Alu repetitive element; mRNA sermonal AA583697
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12140200
On Jan 25, 1995 this sequence version replaced gi:637865.
Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
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Unpublished (1997)
On Apr 14, 1993 this sequence version replaced g1:692704.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 3018699423
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 101)
                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: thyroid gland; Vector: pBluescript Site_1: EcoRI; Site_2: XhoI" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="ATCC (inhost):189984"
/db_xref="taxon:9606"
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Seq primer:

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www-bio.llnl.gov/bbrp/image/image.html

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1991750 106 bp mRNA EST 08-SEP-1999 wt48e01.xl NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510712 3/ similar to contains Alu repetitive element;contains element LTR8 repetitive element;, mRNA sequence.

A1991750 GI:5838578
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                                                                                      Tumor Gene Index
Inpublished (1997)
On Dec 20, 1995 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, CDNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey M
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                     Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 106)
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                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:1088107"
/clone_lib="NCI_CGAP_Kid6"
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                                                                                                                                                                      Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
Insert Length: 1316 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
On May 5, 1995 this sequence version replaced Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 109)
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                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 1316
                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
/db_xref="taxon:9606"
/clone="IMAGE:47310"
/clone_lib="Soares infant brain lNIB"
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/clone_lib="NCI_CGAP_Pan1"
                                                        /organism="Homo sapiens"
/db_xref="GDB:419851"
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                                                                                                                                                                                                                                         Seq F
                                                                                                                                                                                                                                                                                              Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On Jan 24, 1995 this sequence version replaced g1:634306
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy
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3 6 g 18 t
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from
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/db_xref="taxon:9606"
                                                           /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
                                                                                                                    /clone_lib="NCI_CGAP_Pr1"
                                                                                                                                      /clone="IMAGE:1007406"
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AA250812
AA250812.1 GI:1885774
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                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
This clone is available royalty free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
Insert Length: 537 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
On Sep 12, 1996 this sequence version replaced Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced g1:1393355
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Seq primer: -40ml3 fwd.
High quality sequence s
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Emmert-Buck, M.D., Ph.D.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_11b="NCI_CGAP_GC2"
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      AQ200347 109 bp
RPCI11-43B21.TJ RPCI-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are darived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="GDB:7621533"
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/clone="RPCI-11-317H22"
/clone_lib="RPCI-11"
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/note="Vector: pBACe3.6; Site_1:
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Search completed: June 17, Job time: 223032 sec

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JOURNAL
COMMENT
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                      Query Match
Best Local Similarity
Matches 93; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                            17783 AGACCAGCCTGGCTAACATGGCAAAACCCCCATCTCTACTAAAAATACAAAAATTAACCAG 17842
                      17843 GCGTGGTGGTGCACGCCTGTAATCCCCAGCTACTCTGGAGGCTGAGGCA 17890
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62
                                                                                     N
GTGTGGTGGCGCACGCCTGTGATCCCAGCTACTCGGGAGGCTGACGCA 109
                                                                                     Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tlgr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones arailability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or f:
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
Other_GSSs: RPCI11-43B21.TK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
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RPCIll Human Male BAC Library"
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                                                                                                                                                                    Score 84; DB 103;
Pred. No. 0.77;
0; Mismatches 15;
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Perfect score:
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    Issued_Patents_NA:*

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2: /cgn2_6/ptodata/]

3: /cgn2_6/ptodata/]

4: /cgn2_6/ptodata/]

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Match
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6349.604 Million cell updates/sec
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US-08-485-8673C-91
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US-08-481-557C-70
US-08-481-577C-92
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US-08-481-577C-92
US-08-222-177A-430
US-08-451-673C-92
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            65, Appl
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65, Appl
91, Appl
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67, Appl
70, Appl
                                               ; ANTI-SENSE: US-08-481-658B-65
Query Match
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US-08-485-862B-66	US-08-486-756A-66	US-08-477-504A-66	US-08-481-658B-66	PCT-US95-17111A-69	US-08-450-673C-69	US-08-340-426D-69	US-08-454-557C-69	PCT-US95-17111A-60	US-08-450-673C-60	US-08-340-426D-60	US-08-454-557C-60	PCT-US95-17111A-91	US-08-450-673C-91	US-08-340-426D-91	US-08-454-557C-91	US-08-222-177A-166	US-08-222-177A-244
Sequence 66, Appl				69,	69,		69,		60,				Sequence 91, Appl	Sequence 91, Appl	Sequence 91, Appl	Sequence 166, App	Sequence 244, App

ALIGNMENTS

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RESULT 1
US-08-481-658B-65/c
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L
REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: 10-0021.3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorek, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELECHONE: 415-435-2034
TELECAS: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
MOLECULE TYPE: I
MYPOTHETICAL: NO
                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Score Pred.

82.6; DB 4; No. 1.7e-09;

Length 105;

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                                                                                                                              Matches
                                                                                                                                          Best Local Similarity
                                                                                                                                                        Query Match
              16804 CTGACCAACATGGTGAAACCCTGTCTCTACCAAAAATACAAAA 16848
                                                                             16744 ATCCCAGCACTTTGGGAGGCCCAAGGCGGACAGATCACGAGGTCAGGAGTTTGAGACCAGC 16803
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SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
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STREET:
CITY: Tiburon
CITY: California
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                                                                                                                                                     MOLECULE N
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94920
                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                              ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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                                                                                                                         Score 82.6; DB 4;
Pred. No. 1.7e-09;
0; Mismatches 14;
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                                                                                                                                                          Length 105;
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                                                                                                                             Indels
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RESULT

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US-08-485-862B-65/c

; Sequence 65, Application US/08485862B

; Patent No. 5989838
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                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415-435-20:
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          16744 ATCCCAGCACTTTGGGAGGCCAAGGCGGACAGATCACGAGGTCAGGAGTTTGAGACCAGC 16803
                                                                                                                                                                                                                                                                                        16804 CTGACCAACATGGTGAAACCCCTGTCTCTACTAACAAAATACAAAA 16848
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                       APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                               CORRESPONDENCE ADDRESS:
                                                    TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                          105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 0: CLASSIFICATION:
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STREET:
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6 Mariposa Court
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                Leona L.
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Pred. No. 1.7e-09;
0; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6027887
GENERAL INFORMATION:
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Best Local S
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TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvi
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: NN Gene a
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DN
HYPOTHETICAL: NO
ANTI-SENSE: NO
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REGISTION NUMBER: 30,863
REFERENCE_DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 96
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MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: SINGE STRANDEDNESS: S
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APPLICATION: 435

APPLICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                 94104
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                         Version #1.30 (EPO)
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                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                               Sequence 91, Application US/08454557C Patent No. 5830670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: de la Monte, Si
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural
TITLE OF INVENTION: of Al:
                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     16804 CTGACCAACATGGTGAAACCCTGTCTCTACTAACAAAATACAAAA 16848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
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APPLICATION NUMBER: US 08
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0:
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER:
FILING DATE: 07-JUN-
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PRIOR APPLICATION DATA:
                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                STREET: 1100 New CITY: Washington STATE: D.C.
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REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08 FILING DATE: 07-JUN-1995
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STRANDEDNESS: double
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                 COUNTRY: U.S.A. ZIP: 20005-3934
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                                                                                                 ADDRESSEE:
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                                              D.C.
                                                                               E: Sterne, Kessler, Goldstein & 1100 New York Avenue, Suite 600
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86.7%;
                                                                                                                                               Neural Thread Protein Gene of Alzheimer's Disease
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                                                                                                                                                                                                Suzanne
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Pred. No. 1.7e-09;
0; Mismatches 14;
                                                                                                 Fox P.L.L.C
                                                                                                                                                                 Expression and Detection
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

Floppy disk

MEDIUM TYPE: Flop COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI

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REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5948634
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426E
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16794 TGAGACCAGCCTGACCAACATGG 16816
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/454,557C FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                          COUNTRY:
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20005-3934
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1100 New York Avenue, Suite 600
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                                                                                    0609.3840002
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 Mismatches

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Pred. No. 1.8e-06;
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US-08-450-673C-91/c
                                                                                                                                                                                   TOPOLOGY: US-08-450-673C-91
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Best Local Similarity
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                                                                                                         Matches
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16734 CACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGACAGATCACGAGGTCAGGAGTT 16793
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                                                             16734 CACGCCTGTAATCCCAGCACTTTGGGAGGCCCAAGGCGGACAGATCACGAGGTCAGGAGTT 16793
16794 TGAGACCAGCCTGACCAACATGG 16816
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                       NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE, DOCKET NUMBER: 061
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: 1
TOPOLOGY: both
                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                               LENGTH: 84 base pairs TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
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                                          CGACACCAGCCTGATGAACATGG
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1100 New York Avenue, Suite 600
                                                                                                         Conservative
                                                                                                                                                                                                  both
                                                                                                                                                                                                                                                                                                           (202) 371-2600
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                                                                                                       Score 68.6; DB 4;
Pred. No. 1.8e-06;
0; Mismatches 9;
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Pred. No. 1.
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Best Local Similarity
Watches 74; Conserva
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                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-17111A-91
                                                                                                                                                                                                            Sequence 65, Application US/08481658B Patent No. 5955075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 91, Application PC/TUS9517111A GENERAL INFORMATION:
                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   16794 TGAGACCAGCCTGACCAACATGG 16816
                                                                                                                                                                                                                                                                                                                                                                                                                                          16734 CACGCCTGTAATCCCCAGCACTTTGGGAGGCCAAGGCCGACAGATCACGAGGTCAGGAGTT 16793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                             APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14 NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Wands, Jack R.
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CITY: Washington
                                                                                                                                                                                                                                                                                                                               23 CGACACCAGCCTGATGAACATGG 1
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TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
STREET: 6 Mariposa Court CITY: Tiburon STATE: California
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                                                         ADDRESSEE:
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20005-3934
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1100 New York Avenue, Suite 600
                                                                                                                                                                        Zavada, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                           Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.2%; Score 68.6; DB 6;
89.2%; Pred. No. 1.8e-06;
ative 0; Mismatches 9;
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QY 15156 TGGCCTCAAGCGATCCACTTGCCTTTGGCCTCCCAAAGTGCTAGGAT 15201
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Best Local Similarity 82.1%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/08477504A Patent No. 5972353
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15096 TITTTGTATTAGTAGAGATGGGGTTTCGCCATGTTGGCCAGGCTGGTCTCGAACTCC 15155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-435-072/
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APPLICATION NUMBER: US 08/
FILING DATE: 15-7UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE NUMBER NO
                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
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                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: D-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                             STREET: 6 Mari
CITY: Tiburon
STATE: Califor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
ZIP: 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/481,658B FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           COUNTRY: U
ZIP: 94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TGACCT--TGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                 6 Mariposa Court
                                                                                                                                                                                                             USA
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Pred. No. 1.4e-05;
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APPLICATION NUMBER: US 08/260,190 FILING DATE: 15-JUN-1994 ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

30,863

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; ANTI-SENSE: NO
US-08-477-504A-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15096 TTTTTGTATTATTAGTAGAGATGGGGTTTCGCCATGTTGGCCAGGCTGGTCTCGAACTCC 15155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
             TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO:
                                           NAME: Lauder, Leona L.
REGIZION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2334
                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
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                                                                                                                                                                                                 APPLICATION NUMBER: US/08/486,756A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                   94920
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                                                                                                                                                                                                                                                                                                                                                                                      California
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82.1%;
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                                                                                              30,863
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                                                                                D-0021.3C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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; TOPOLOGY: linear; MOLECULE TYPE: DNA; HYPOTHETICAL: NO; ANTI-SENSE: NO US-08-486-756A-65
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Patent No. 5989838
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Best Local Similarity
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                                                                                                                                                                                                                                            CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L
                                                                                                                                    REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
ANTI-SENSE:
            MOLECULE TYPE: DI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             NAME: Lauder, Leona L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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CITY: Tiburon
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                                               TOPOLOGY:
                                                                   STRANDEDNESS:
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                                DNA (genomic)
                                                                 single
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82.1%;
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                                                                                                                                                                                                                               30,863
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Pred. No. 1
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US-08-787-739-65
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Patent No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15156 TGGCCTCAAGCGATCCACTTGCCTTGGCCTCCCAAAGTGCTAGGAT 15201
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                                                                                                                TELEFAX: 415-981-0332
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
                                                                                                                                                     REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/485,863 FILING DATE: 07-JUN-1995
                              TOPOLOGY:
                                             STRANDEDNESS:
                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 24-JAN
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6027887
                                                               nucleic acid
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                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Leona L. Lauder
369 Pine Street, Suite
                                                                                105 base pairs
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DNA (genomic)
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24-JAN-1997
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0; Mismatches 17;
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RESULT 15
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                                                                                                                                       Query Match 0.2%;
Best Local Similarity 85.7%;
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Best Local Similarity
Matches 87; Conserv
                                                                             15081 ACCATGCCTGGCTAATTTTTGTATTATTAGTAGAGATGGGGTTTTCGCCCATGTTGGCCAGG 15140
                             15141 CTGGTCTCGAACTCCTG 15157
                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0:
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
61
                                                                                                                                                                                                                                                                                                                   TELEFAX:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                      TYPE:
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Pred. No. 0.00018;
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Search completed: June 17, 2000, 10:50:11 Job time: 251741 sec

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Title:
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Listing first 45 summaries
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Maximum DB seq length: 110
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18001
1 GATAGGCTCACTTCTAACCA......CCATCCAGCTTCTCACTCCT 18001
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-600.987 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

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BASE COUNT
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ORGANISM
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AUTHORS
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HSLDLRN2/c
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HSU67803/c
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87161901
See X052
Data kin
                                                      Direct Submission
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology,
Submitted (22-AUG-1996) Human Genetics and Molecular Biology,
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, Center, Jocation/Qualifiers
                                                                                                                                                                                J. MOL. E
97415756
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U67803.1 GI:2289917
Alu.
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism fc the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
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Alu repetitive sequence; low density lipoprotein receptor
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Shaikh,T.H., Roy,A.M., Kim,J., cDNAs derived from primary and
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Shalkh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human small cytoplasmic
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu2"
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/db_xref="taxon:9606"
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HUMALCE221/c
                                KEYWORDS
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Matches 91
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1 (bases 1 to 103)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cel post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
Location/Qualifiers
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Human carcinoma
M87896
                                                                          Human LDL-receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M87896.1 GI:174874
Homo sapiens
                                Alu repetitive sequence;
                                          X05248.1 GI:34334
                                                               density lipoprotein.
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                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/rpt_type=dispersed
39 c 30 g
                                                                                                                                                                                                                                                                                                                      /dev_stage="embryo"
/sex="male"
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27 c 33 g 1
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Pred. No. 0.00069;
0; Mismatches 11
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Pred. No. 0.00024;
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Alu RNA transcript,
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clone CE221.
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Best Local S
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                12712 TTTTTTTTGACTGAGTCTTGCTCTGTCTCACAGGCTGGAGTGCAGTGGGATCTCGGC 12771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11274 GTAGCAGGGTCTACAGGCATGTGCCACCACCCCGGCTGTTTTTGTA 11320
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TTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCTCGGC 48
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1 (bases 1 to 108)

Horsthemke, B., Beisiegel, U., Dunning, A., Havingz, J.R., Williamson, R. and Humphries, S.

Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                          Alu RNA transcripts in human embryonal carcinoma cells. post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens male embryo carcinoma cDNA to Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          M87924.1 GI:174871
Alu repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human carcinoma cell-derived Alu RNA transcript,
                                                                                                                                                                                                                                                                                                                                                           Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
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                                                                Conservative
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/db_xref="taxon:9606"
complement(<1. .65)
/note="Alu repeat"
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38 c 20 g 29 t
                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                           /tissue_type="carcinoma"
30 c 35 g 1
                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                            /cell_line="NTera2D1"
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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lone CE162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13471 TIGGCTCATIGCAACCTCTGCCTCCTGGGTTCAAGTGATTCTCCTGACTCAGCCTCCCGA 13530
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Horsthemke,B., Beisiegel,U., Dunning,A., Havinga,J.R., Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
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In the defective LDL-receptor gene the deletion occurred between
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading fram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S. Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism the defect in a patient with familial hypercholesterolaemia the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familial hypercholesterolaemia in the defect in a patient with familia hypercholesterolaemia in the defect in a patient with familia hypercholesterolaemia in the defect in a patient with familia hypercholesterolaemia in the defect in a patient with familia hypercholesterolaemia in the defect in a patient with familia hypercholesterolaemia in the defect in a patient with familia hypercholesterolaemia in the defect in a patient with the defect in a patient with the defect in a patient with the defect in the defect in the defect in a patient with the defect in the defec
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
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1 (bases 1 to 108)
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                                                                                                                                                                                                                                                                             Homo sapiens
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61

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                                                  GCGGGAGGATCACTTGAACCTGGGAGGCAGAGATTGCAATGAGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See X05250 for corresponding normal gene sequence In the defective LDL-receptor gene the deletion ocurred between two alu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R., and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
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90; Conserv
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1 (bases 1 to 108)
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Pred. No. 0.0034;
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                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)

1 (bases 1 to 91)

Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                        HUMUT8164A 91
Human STS UT8164,
L30244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 108)
Shaikh, T.H., Kim, J.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
U67804
Genetic and physical mapping of simple sequence sequence tagged sites from the human genome Unpublished (1994)
Submitted by: Utah Center for Human Genome Resea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shaikh, T.H., Roy, A.M., Kim, J., cDNAs derived from primary and
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                                                                                                                                                                                                                                                                                                      DNA STS 29-DE primer bind, sequence tagged site.
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Pred. No. 0.0069;
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                                                                                                                                                                                                                                                   Direct Submission
Submitted (12-FEB-1991) F.L. Aldridge,
Alderley Park, Macclesfield, Cheshire,
2 (bases 1 to 103)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cycles Denaturation Annealing Extension C 10 sec. 56 C 10 sec. 72 C 20 sec. 30 52 C 10 sec. 72 C 20 sec. Mg++: 1.50 mM Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e-mail: sts@corona.med.utah.edu
Primer A: AGAGGTTGCAGTGAACCAA
Primer B: TTTTTCCCCCTCTACTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Utah, Dept. of Human Genet
2160 Eccles Institute of I
Salt Lake City, UT 84112
                                                                                                                                                                                                         Butler,R., Riley,J.H., Ogilvie,D.J., Anand,R., Buxton,J., Davies,J., Johnson,K. and Markham,A.F.
Two sequence-tagged sites defining the ends of a 380 kb YAC
                                                                                                                                                                                                                                                                                                                                                                                                                      Human sequence tage
X57789
X57789.1 GI:23938
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1 (bases 1 to 103)
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                                                                                                                                                                                                                                                                                                                Aldridge, F.L.
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Location/Qualifiers
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/db_xref="taxon:9606"
10. .28
                          /chromosome="19q13"
/germline
/clone_lib="YAC library: ICI"
/clone="8IC8"
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                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                             ACCCGACTTGGCCTCCCAAAGTGCTGGGATTACAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85;
                                                                                      Human sequence
X57789
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J. Mol. Biol. 271 (2), 222-234 (1997)
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Primates; Catarrhini; Hominidae; Homo.
                             Homo sapiens
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RESULT 14
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GTTTCGTCATGTTAGCCAGGCTGGTCTTGAACTACTGAGCTCGCAATCCTCCTGCCTTGG
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1 (bases 1 to 110)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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Davies,J., Johnson,K. and Markham,A.F.
Two sequence-tagged sites defining the ends of a 380 kb YAC clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMALCE43 110 bp ss-RNA PRI Human carcinoma cell-derived Alu RNA transcript,
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/db_xref="taxon:9606"
/chromosome="19q13"
                                                                                                                                                                /tissue_type="carcinoma"
31 c 34 g 1
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/db_xref="taxon:9606"
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CTGAGTAGCTGGGATTACA-GCATGCGCCACCACNCCTGGCTTTTTAT 1
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Matoba,R., Okubo,K., Hori,N., Fukushima,A. and Matsubara,K.
The addition of 5'-coding information to a 3'-directed cDNA library improves analysis of gene expression
Gene 146 (2), 199-207 (1994)
94357437
                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo Matoba, Osaka University, Institute for Molecular and Cellular in 1-3, Yamada-oka, Suita, Osaka 565, Japan (E-mail:matoba@inherit.imcb.osaka-u.ac.jp, Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 108)
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Human HepG2 partial cDNA,
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07747-5-2321
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                                                                                                                                                                                                                    /sex="Male"
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/clone_lib="Kiseru"
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X12095/c
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          ID DE PRESENTATION OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PT New alleles and allelic ladder mixtures - useful as a control sample PT for DNA profiling in forensic environments
PS Claim 1; Page 39; 52pp; English.

CC This sequence represents an allelic ladder, used in the allelic ladder CC one of the invention. The allelic ladder mixture comprises at least CC one of the following allelic ladders: (1) at least one allele for locus CC (1) at least one allele for locus EUGHAPA31/A; (ii) one allele for locus HUMHDO1; (ii) at least one allele for locus D1851179; (iv) at least one allele for locus business of least one allele for locus D20511; and (v1) an allele for locus D18511; and least one allele for locus D18511; and (v1) an allele for locus CC (v) at least one allele for locus D20511; and (v1) an allele for locus D18511. The alleles or allele for locus D20511; and (v1) an allele for locus CC comparison with a sample DNA profile, when the profile is based on CC analysis of at least one loci of HUMWTRA31/A, HUWHDO1, D851179, CC HUMPTRAA,FCA, D21511, D18551 or AMG (amelogenin sex test). DNA profiling cis useful in anthropological, paternity, maternity, crime detection and cother forensic environments. The new allelic ladders have an improved CC range and coverage of DNA, and include a number of rare alleles which CC offers improved identification of an unknown sample.
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Best Local S
Matches 81
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Hudson T, Lander ES, Wang D;
WPI; 98-286974/25.
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome determining polymorphic forms for use in e.g. forensics, testing or phenotypic typing for disease Claim 1; Page 219; 310pp; English.
X10269-X12937 are human DNA fragments which contain biall
                                                                                                                                                                                         14-MAY-1998.
05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED) WHITEHEAD INST BIOMEDICAL RES
Hudson T, Lander ES, Wang D;
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Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Human biallelic; human; forensic; paternity testing; disease; Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UKHO-) UK SEC STATE HOME DEPT.
Arnold CD, Barber MD, Burke T, Gill P, Gillbard
Griffiths RA, Haywood MD, Johnson PE, Smith CD,
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30-DEC-1998.
30-DEC-1998; 305120.
29-JUN-1997; GB-013597.
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Allelic ladder; human; HUMVWFA31/A; HUMTHO1; D8S1179; HUMFIBRA/FGA; AMG;
D21S11; D18S51; forensic testing; DNA profiling; amelogenin sex test; ss
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X01323;
14-APR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment; marker;
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Pred. No. 0.
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contain biallelic polymorphic
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the appropriate IUPAC-IUB ambiguity code. These fragments can be used in CC methods for determining polymorphic forms in an individual for use in CC e.g. forensics, paternity testing or for phenotypic typing for diseases cuch as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, CC muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial CC hypercholesterolemia, polycystic kidney disease, hereditary CC spherocytosis, von Willebrand's disease, therous sclerosis, hereditary camemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danios CC syndrome, osteogenesis imperfecta, acute intermittent porphyria, CC autoimmune diseases, inflammation, cancer, diseases of the nervous cystem, infection by pathogenic microorganisms, and characteristics such cas longevity, appearance (e.g. baldness, obesity), strength, speed, CC endurance, fertility, and susceptibility or receptivity to particular CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid cegments can also be used to produce medicaments for the treatment or CC prophylaxis of such diseases.

28 Sequence 108 BP; 19 A; 23 C; 28 G; 37 T;
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         Claim 1; Page 1720; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA ilbraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA, species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsubara K, Okub
WPI; 95-206931/27.
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W09514772-A1.
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Pred. No. 0
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07-NOV-1996

(first entry)

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                                          RESULT
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Sequence 103 Bp; 33 A; 21 C; 25 G; 23 T;
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Best Local
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T25009 standard;
T25009;
                                                                                                     5916 TCTCAGCTCACTGCAGCCTTGAACTCCAGGGCTCAAGCAATC 5957
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504
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WPI; 95-206931/27.
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                                                                                     TCATAGCTCACTGTAACACCCAAACTCCTGGACTCAAGTGATC
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79; Conser
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77.58;
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77.88;
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Claim 1; Page 1748; 2245pp; Japanese.

Claim 1; Page 1748; 2245pp; Japanese.

Claim 2; Page 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                             Homo sapiens.
W09514772-A1.
01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
MALSUBARA K.
OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15086 CATGATCTCAGCTCACTGCAGCCTCCGGCCTCCCGGGTTCAAGAGAT 15131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; cloning
cell typing; a
Homo sapiens.
WO9514772-A1.
                                                                                                                                                                                                                                                                                                                 Gene signature; messenger RNA;
human; cloning; mapping; non-bi
cell typing; abnormal cell fund
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                          Identifying gene signatures in for diagnosis of abnormal cell reflects relative abundance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying gene signatures in 3'-direct for diagnosis of abnormal cell function, reflects relative abundance of corresp.
                                                                                                               Matsubara K, Okub
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                     Human gene signature HUMGS09078.
                                                                                                                                                                                                                                                                                                                                                                                                             T26828;
14-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          T26828 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 95-206931/27.
                  tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (окив/) окиво к.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 CGTGACCATGGCTCACTGCAGCCTTGGCCTCATGGGCTCAGGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
Page 2182; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                   re; messenger RNA; mRNA; relative abundance; frequency; ng; mapping; non-biased library; diagnosis; detection; abnormal cell function; ss.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.3
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3'-directed human cDNA library - e.g. function, by preparing cDNA that corresp. mRNA in specific human
                                                           3'-directed human cDNA library -
function, by preparing cDNA that
                                          corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
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                                               mRNA in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                            specific human
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RESULT
T24892
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So sequence 108 BP; 18 A; 33 C; 23 G; 28 T;
Sclaim 1; Page 1720; 2245pp; Japanese.

Claim 1; Page 1720; 2245pp; Japanese.

Claim 1; Page 1720; 2245pp; Japanese.

Claim 2; Page 1720; 2245pp; Japanese.

Claim 3; Page 1720; Page 1837 "GS" sequences

Claim 2; Page 1720; Page 1837 "GS" sequences

Claim 3; Page 1720; Page 1837 "GS" sequences

Claim 2; Page 1720; Page 1837 "GS" sequence

Claim 3; Page 1720; Page 1837 "GS" sequence

Claim 2; Page 1720; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo sapiens.

W09514772-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OKUB/) OKUBO K.
Matsubara K, Okubo K;
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T24892 standard; cDNA to mRNA; 100 BP. T24892;
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene signature HUMGS06998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1996 (first entry)
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0;

Query Match

0

Score 60.2;

DB

1;

Length 100;

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RESULT 9
1720927/c
1D 720927; standard; cDNA to mRNA; 10
AC 720927;
DF 24-7UL-1996 (first entry)
DF 24-7UL-1996 (first entry)
DF Human gene signature HUMGS02180.
KW human; cloning; mapping; non-bias
KW cell typing; abnormal cell functi
OS Homo sapiens.
PN W09514772-A1.
PD 01-7UN-1993; JP-355504.
PA (OKUB/) OKUBO K;
PF 11-NOV-1993; JP-355504.
PA (OKUB/) OKUBO K,
PA (OKUB/) OKUBO K,
PA (OKUB/) OKUBO K,
PI Matsubara K, Okubo K;
PI Identifying gene signatures in 3'
PT of diagnosis of abnormal cell fur for diagnosis of abnormal cell fur reflects relative abundance of cc tissues
PS Claim 1; Page 758-759; 2245pp; Ja
CC a single-stranded DNA (or its com cc double-stranded DNA) which compring given in T19001-T26837 and which compring given in T19001-T26837 and which compring given in T19001-T26837 and which compring given in T1901-T26837 and which compri
   RESULT 1
T21566/c
ID T215
AC T215
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DT 03-A
DE Huma
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Claim 1; Page 758-759; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. Couble-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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Best Local S
Matches 73
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Human gene signature HUMGS02944. Gene signature; messenger RNA; m
                                                                T21566 standard; cDNA to mRNA; T21566; 03-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                      4322 TGTAATCCCAGCTACTCAGGAGGCTGAAGCGGGAGGATC 4360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4262 ATGGTGAAACCTCATCTCTACTAAAAATACAAAAAGCTAGCCAGGCGTGGTGGTGCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGAGAAATACTGTCCCTACTNAAAATACNAAAATCAGCTGGACATGGTGGCACACACC
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   RNA; mRNA; relative abundance; frequency;
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Pred. No. 1
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                                                                                                                                    87
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                                                                                                                                    ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 11
Q95218/c
ID Q95218 standard; DNA; 85 BP
AC Q95218;
DT 08-FEB-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (dene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 87 BP; 35 A; 21 C; 16 G; 13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 68
                                                                                                                                                                                                    Synthetic.

W09517522-A2.

29-JUN-1995.

21-DEC-1994; G02789.

21-DEC-1993; GB-026052.

(UYLE-) UNIV LEICESTER.
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11-NOV-1994; J01916.
12-NOV-1993; JP-35504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13620
Claim 26; Page 29; 51pp; English. (STR) corresponding to the 2nd part of wg3b10. The STR can be used for treatment and diagnosis in human and veterinary medicine, partic. for genetic characterisation, mapping, linkage studies and analysis/diagnosis of acquired disease
                                                                                                                                                                                                                                                                                                                          Simple tandem repeat (STR)
Simple tandem repeat; STR;
characterisation; mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                   Identifying simple tandem repeat loci in DNA - by screening DNA library to enrich for fragments contg. the repeats before cloning and rescreening, also simple tandem repeats for treatment or
                                                                                                                                                                       Armour J, Jeffreys AJ;
WPI; 95-240682/31.
                                                                                                                                                                                                                                                                                                              second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 914;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; cloning; mapping; non-biased library; diagnosis; detection;
typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTCAAACTCCTGACCTCAAGTGATC 13645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCTGGGTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGACCAGGCTGG 13619
                                                                                                                                                                                                                                                                                                              part; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2245pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.3%;
79.1%;
                                                                                                                                                                                                                                                                                                                          corresponding to the 2nd part of wg3b10, wg3b10; treatment; genetic; diagnosis; linkage studies; analysis; alleles;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58.4;
Pred. No. 1
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11396

TCAGTCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCAC

TAAGCCTCCYAAAGTGCCAGGATTATAGGTGTGAGTCAC

GAGTCTTGCTATGTTTCCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCC

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X120857
ID 20857
ID 20857
ID 20857
AC 2120857
AC 212085
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                                                                                                                                                                                                                                                                                                                           PT New isolated nucleic acid segments from the human genome - used for PT New isolated nucleic acid segments from the human genome - used for PT determining polymorphic forms for use in e.g. forensics, paternity PT testing or phenotypic typing for disease
PS Claim 1; Page 218; 310pp; English.

CC X10269-X12937 are human DNA fragments which contain biallelic polymorphic CC Markers which have been isolated using the primers represented in CC commission of the base occupying the polymorphic site is indicated by CC the appropriate IUPAC-IUB ambiguity code. These fragments can be used in CC e.g. forensics, paternity testing or forms in an individual for use in CC e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, CC muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos CC syndrome, osteogenesis imperfecta, acute intermittent porphyria, cc autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such can be intered the colonic colonic colonic polyposis, expenditury annearrance (or a haldness obseity) strength, speed.
   Query Match
Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 67; Conser
                                                                                                                                                                                                                as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human biallelic polymorphic DNA fragment EST98276c. Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5832
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W09820165-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 98-286974/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WHED ) WHITEHEAD INST BIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-1996; US-030455.
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                                                                                                                                                                                         prophylaxis of
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                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marker;
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      Conservative
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                                                                                                                                                            diseases.
22 A;
                                0.3%;
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Score 57; DB Pred. No. 2.8; 1; Mismatches
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Pred. No. 2.5;
0; Mismatches
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                                2.8;
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                                                          Length 100
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PT New isolated nucleic acid segments from the human genome - used for PT New isolated nucleic acid segments from the human genome - used for PT New isolated nucleic acid segments for use in e.g. forensics, paternity PT testing or phenotypic typing for disease PS Claim 1; Page 219; 310pp; English.

CC Markers which have been isolated using the primers represented in CC markers which have been isolated using the primers represented in CC markers which have been isolated using the primers represented in CC e.g. forensics, paternity testing or forms in an individual for use in CC e.g. forensics, paternity testing or forms in an individual for use in CC e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial CC hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos cystem, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular cromps of such diseases.

CC segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.

Seguence 100 BP; 21 A; 25 C; 22 G; 31 T;
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                                                                                                                                                                                                                                                        RESULT
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                   11396
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Polymorphism; biallelic; human; forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
treatment; marker; ss.
                                                                                                      Gene signature; messenger RNA; mRNA; relative abundance human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1999
              01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                     Homo sapiens.
W09514772-A1.
                                                                                                                                                              Human gene signature HUMGS04188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
Hudson T, Lander ES, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X12086 standard; DNA; 100
                                                                                                                                                                                 01-OCT-1996 (first entry)
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(MATS/)
                                                                                                                                                                                                                   [22572 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                           TMAGCCTCCTAAAGTGCCAGGATTATAGGTGTGAGTCAC
                                                                                                                                                                                                                                                                                                                             TCAGTCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCAC 11434
                                                                                                                                                                                                                                                                                                                                                                                  GAGTCTTGCTATGTTTCCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCC
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MATSUBARA K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lander ES, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                            relative abundance;
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2.8;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                            Claim 1; Page 1224; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthatis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene signature HUMGS04510.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5872
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                                                                                                                                                                                                                                                                                                                                Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                              Matsubara K, Okub WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
WO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsubara K, Okub
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T22836 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reflects relative abundance of corresp. mRNA in
different mRNAs in the particular tissue
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                            s constructed so as to reflect accurately the relative abundance
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Pred. No. 3;
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CC The appearance frequency of a given GS in a cDNA library can be CC determined (esp. using primers and probes derived from the GS CC sequences) as a means of diagnosing abnormal cell function or for CC recognising different cell types.

SQ Sequence 82 BP; 26 A; 25 C; 14 G; 17 T;

Ouery Match
Best Local Similarity 80.5%; Pred. No. 3.4;
Matches 66; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Oy 4542 TTTAAGTTCCTGGGTACAAGTACAGGATCTGCAGGTTTGTTACATAGGTAAACGTGTGCC 4601

Db 82 TTTAAGTTCTGGGGTACAACTACAGGATCTGCAGGTTTGTTATGCAGGGTAAATGTGTGCC 23

Oy 4602 ATGCTGATTTGCTGCACCTATC 4623

Oy 4602 ATGCTGATTTGCTGCACCTATC 4623

Oy 4602 ATGCTGATTTGCTGCTCCTCAGATC 1

Search completed: June 17, 2000, 11:43:23

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 June 17, 2000, 02:34:25; Search time 13753.1 Seconds (without alignments) 5305.117 Million cell updates/sec
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On Dec 3, 1996 this sequence version replaced gi:1
                                                                                                           zr25h02.sl Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664467 3' similar to contains Alu repetitive element; contains element LTR1 repetitive element; mRNA sequence.
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                                          Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                   Lennon, G., Marra, M.,
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AA078003 7H12D08 C

AQ412658 RPCI-I1-2

B32951 HS-1016-A1-

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AQ200347 RPCI-11-43

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1 (bases 1 to 106)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu, NCI human EST Project
                                                                                                                          Unpublished (1997)
On Sep 12, 1996 this sequence version
Contact: Wilson RK
Washington University School of Medici
4444 Forest Park Parkway, Box 8501, St
Tel: 314 286 1810
Fax: 314 286 1810
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This clone is available royalty-free thro
TMAGE Consortium (info@image.lln1.gov) fo
Insert Length: 1127 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 102.
Location/Qualifiers
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA703692
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Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:9606"
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/clone_lib="Stratagene NT2 neuronal precursor
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                                                                                                                     Insert Length: 1661 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 87.
                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 12, 1996 this sequence version replaced gi:1393355 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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1 (bases 1 to 107)
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nk42b11.s1 NCI_CGAP_GC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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EST.
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                                                                                                                                                                                                                     cDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
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/dev_stage="NNT neurons"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: Cloned unidirectionally. Primer: Oligo dT.
NhoI; Cloned unidirectionally. Primer: Oligo dT.
Siferentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; Uni-&AP XR Vector; -5' adaptor sequence: 5'
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/clone="IMAGE:1140858"
/clone="IMAGE:1016157"
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                                                                                                                                                                                                        Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                  Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or figure from the first page in the first page.

Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M.D., Rounsley, S.D., Field, Golden, K., Berry, K., Granger, D., Venter, J.C.
Use of BAC End Sequences for Sequ
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/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
28 c 30 g 15 t
                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:7501163"
/db_xref="taxon:9606"
/clone="RPCI-11-4A12"
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                                                                          /sex="Male"
                                                                                             /clone_lib="RPCI-11"
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., Wible,C., de Jong
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                            TCAGCCTCCCAAAGTACTTGGATTACAGGCGTGAGCCACTGCTCCC
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Other_GSSs: RPCII1-134I4.TJ
Contact: Shaying Zhao, William Nierman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ386882.1 GI:4357905
GSS:
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or figures arch Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
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95; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="GDB:7551267"
/db_xref="taxon:9606"
/clone="RPCI-11-13414"
/clone=lb="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/RPCII1 Human Male BAC Library"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                           AQ386882.1
GSS.
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RPCI11-134I4.TV RPCI-11
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Clones are derived from the human BAC library RPCI-11. For BAC

Clones are darived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:
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Eukaryota;
                         Homo sapiens
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Use of BAC End Sequences
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/db_xref="GDB:762153"
/db_xref="taxon:9606"
/clone="RPCI-11-317H22"
/clone_lbb="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
/note="Lymphocytes"
/n
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Metazoa; Chordata;
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Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Other_GSSs: RPCIII-13414.TJ
Contact: Shaying Zhao, William Nies
Department of Eukaryotic Genomics
The Institute for Genomic Research
            Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                 AQ544957 106 bp DNA CITBI-E1-2629N2.TF CITBI-E1
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are darlability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lifto@resgen.com). BAC end search page:
                                                                                                                            Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 106) 2hao, S., Adams, M.D., Nierman, W., Malek, J.,
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Seq primer: T7
Class: BAC ends.
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Use of BAC End Sequences
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Use of BAC End Sequences from CalTech Libraries
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301 838 0200
301 838 0208
 Medical Center Dr.,
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/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
26 c 38 g 20 t
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/clone="RPCI-11-13414"
/clone_11b="RPCI-11"
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genomic clone 2629N2,
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                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy ProTumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA897366 110 bp mRNA EST 04-JJ am06h02.sl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone IMAGE:1466067 3' similar to contains Alu repetitive ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                    On Jan 19, 1998 this sequence version replaced gi:2150764. Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
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/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not T; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="sperm"
/note="vector: pBeloBAC11; Site_1:
CalTech Human BAC Library D"
26 c 36 g 18 t
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/db_xref="taxon:9606"
/clone="2629N2"
                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1466067"
                                                                                       /clone_lib="Soares_NFL_T_GBC_S1"
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nx08b05.sl NCI_CGAP_GC3
similar to contains Alu
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
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On Jan 19, 1998 th
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement:
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                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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Procurement: Christopher A. Moskaluk, M.D.,
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/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3
                                                                                                                                 /clone="IMAGE:1255473"
/clone_lib="NCI_CGAP_GC3"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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             AGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCCACTA 8233
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95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockvill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Other_GSSs: 345K02.TP 345K02.TPB
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345K2.TVB CIT978SKA1
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are available from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a BAC End
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Adams,M.D., Kelley,J.M.,
                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                      /cell_type="Fibroblast",
/note="Vector: pBACI08L; Site_1:
CalTech Human BAC Library A1"
30 c 31 g 24 t
                                                                                                                                                                                                                                                                               /clone_lib="CIT978SKA1"
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                              /clone="A-345K02"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                             AA244245 110 bp
nc07a04.sl NCI_CGAP_Prl
similar to contains Alu
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Class: BAC ends.
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Tel: 301 838 0200
Fax: 301 838 0208
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Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 109)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Other_GSSs: 345K02.TP 345K02.TPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams,M.D., Kelley,J.M., Rounsley,S.R. and Venter,J.C. Use of a BAC End Sequence Database for Sequence~Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       survey sequence.
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345K2.TVB CIT978SKA1
                                                                                        Homo sapiens
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Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Fibroblast"
/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
CalTech Human BAC Library A1"
a 30 c 31 g 24 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="CIT978SKA1"
/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                             mRNA EST 20-AUG-1997 HOMO Sapiens cDNA clone IMAGE:1007406 repetitive element;, mRNA sequence.
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A-345K02, gen
            Project (CGAP),
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QY 13472 TGGCTCATTGCAACCTCTGCCTCCTGGGTTCAAGTGATTCTCCTGACTCA 13521
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
                                                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence. AQ003188
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RPCI11-1D10.TPN RPCI-11
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On Jan 24, 1995 th
                                                                                       Venter, J.C.
Use of BAC End Sequences for
                                                                                                                                               Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bas
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C.,
                                                                                                                                                                                                                                                                                                       Homo sapiens
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Similarity 86.4%;
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act: Robert Strausberg, Ph.D.
(301) 496-1550
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//dev_stage="45 years old"
//lab_host="pHHOB"
//lab_host="pHHOB"
//note="vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
//note="vector: pAMP10; Site_11: Not1; On 50 ng of
Strand cONA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
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26 c 28 g 38 t
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/db_xref="taxon:9606"
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                              GI:3030392
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C., de Jong,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACCTCGTGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAG 12976
                                                                                                                                       Unpublished (1997)
on Sep 12, 1996 this sequence version replaced g
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mdadams@tlgr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 107) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: SP6
Class: BAC ends
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CONA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                      Tumor Gene Index
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nk42b11.s1 NCI_CGAP_GC2
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                                                                                                                    cDNA Library Preparation: Stratagene, Inc.,
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
27 c 26 g 35 t
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/clone="RPCI-11-1D10"
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/db_xref="GDB:7500081"
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Homo sapiens cDNA clone IMAGE:1016157
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                                                                                                                    David B. Krizman,
                                                                                                                                                                 Ph.D., Michael
                       information
                                                 Sequencing Center
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                                                TGGTGTGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCACGAGAATCACTTGAACCT 48
GGGAGGCAGAGCTTGCAGTGAGCTGAGATTGAGCCACTGCACTCCAG
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                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                           quality sequence stop:
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                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1016157"
/clone_11b="NCI_CGAP_GC2"
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87.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM nucleic - nucleic search, using sw model
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_b/ptodata/

2: /cgn2_b/ptodata/

3: /cgn2_b/ptodata/

4: /cgn2_b/ptodata/
5: /cgn2_b/ptodata/
6: /cgn2_b/ptodata/
7: /cgn2_b/ptodata/
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length: 110
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18001
1 GATAGGCTCACTTCTAACCA.....CCA:
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/cgn2_6/ptodata/1/ina/5D_COMB.seq: *
/cgn2_6/ptodata/1/ina/5C_COMB.seq: *
/cgn2_6/ptodata/1/ina/FCTUS_COMB.seq: *
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
   GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd.
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US-08-487-504A-65
US-08-485-862B-65
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US-08-454-557C-91
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US-08-454-557C-91
US-08-454-557C-91
US-08-454-557C-91
US-08-450-673C-91
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Best Local Similarity
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US-08-471-907A-42	US-08-088-658-42	PCT-US95-17111A-57	US-08-450-673C-57	US-08-340-426D-57	US-08-454-557C-57	PCT-US95-17111A-60	US-08-450-673C-60	US-08-340-426D-60	US-08-454-557C-60	PCT-US95-17111A-69	US-08-450-673C-69	US-08-340-426D-69	US-08-454-557C-69	US-08-332-766A-44	PCT-US95-17111A-70	US-08-450-673C-70	US-08-340-426D-70
Sequence 42, Appl	Sequence 42, Appl	Sequence 57, Appl	Sequence 57, Appl	•	-	-	-	-	-	Sequence 69, Appl	•	•	Sequence 69, Appl	•	Sequence 70, Appl	Sequence 70, Appl	Sequence 70, Appl

ALIGNMENTS

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US-08-481-658B-65
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US-08-481-658B-65
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                                                                                                                   TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0!
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zavada, Jan
APPLICANT: Pastorekova
            HYPOTHETICAL:
ANTI-SENSE:
                                        MOLECULE TYPE:
                                                                                                                                                                   TELEPHONE: 415-435-2034
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                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                 NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                       nucleic acid
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SYSTEM: PC-DOS/MS-DOS
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Score 78.4; DB Pred. No. 7e-08;

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RESULT
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INFORMATION FOR SEQ ID NO: 6/
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
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Best Local
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                                                          12928 TGACCTCGTGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGAT 12971
                                                                                                                    12868 TTTTTGTATTTTTAGTAGAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCCGATCTCC 12927
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                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                          62
                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/477,504A FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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                                                                                                      2 TTTTTACATCTTTAGTAGAGAGAGGGTTTCACCATATTGGCCAGGCTGCTCCAAACTCC 61
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                                          TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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                                                                                                                                                                              Similarity
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 7e-08;
0; Mismatches 16;
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                                                                                                                               Sequence 65, Application US/08485862B Patent No. 5989838 GENERAL INFORMATION:
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                               12928 TGACCTCGTGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGAT 1297:
                                                                               APPLICANT: Zavada, Jan
APPLICANT: Pastorekova,
APPLICANT: Pastorek, Ja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, V CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/486,756A
                                 CORRESPONDENCE ADDRESS:
                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                    ADDRESSEE:
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6 Mariposa Court
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                                                                                 Pastorekova, Silvia
Pastorek, Jaromir
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                  Leona L.
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                                                                                                                                                                                                                                                                                                                                                                                                0.4%;
                                                 MN Gene and Protein 86
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MN Gene and Protein
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                    Lauder
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                                                                                                                                                                                                                                                                                                                                                                                                Score 78.4; DB 4; Pred. No. 7e-08;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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us-08-787-739-65
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Matches
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                     Patent No. 6027887
GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12868 TTTTTGTATTTTTAGTAGAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCC 12927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12928 TGACCTCGTGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGAT 12971
              COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, S:
                                                                                                                                                                                                                          APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                             65,
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                Release #1.0, Version #1.30 (EPO)
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                                                                                                                                                                             Suite 610
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COMPUTER READABLE FORM:
                  COUNTRY:
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US-08-481-658B-65/c ; Sequence 65, Application US/08481658B ; Patent No. 5955075
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: LAUDET, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12868 TITTTGTATTTTTAGTAGAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCC 12927
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                12928 TGACCTCGTGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGAT 12971
STREET:
STREET:
CITY: Tiburon
CTATE: California
                                                                                                                                      APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene
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LENGTH: 105 base pairs
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PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 08/481,658
FILING DATE: 07-JUN-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                            62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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                                                              6 Mariposa Court
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                                                                                  Leona L. Lauder
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                                                                                                                                            MN Gene and Protein
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Pred. No. 7e-08;
0; Mismatches 16;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:

MEDIUM TYPE: COMPUTER: II

: Floppy disk
IBM PC compatible

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; TOPOLOGY: linear
; MOLECULE TYPE: DNP
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-481-658B-65
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TELEPHONE: 415-435-0727
TELEPAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
FILING LALE CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: US 08/260,190
APPLICATION NUMBER: US 08/260,190
APPLICATION NUMBER: 15-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zavada, Jan
APPLICANT: Pastorckova, Silvia
APPLICANT: Pastorcek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
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                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                          COUNTRY:
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o. 5972353
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DEDNESS: single
                                                                                                                                                                                                                                                                                              California
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6 Mariposa Court
                                                                                                                                                                                                                                                                            USA
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                                                                                                                    US/08/477,504A
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RESULT 8
US-08-486-756A-65/c
; Sequence 65, Application US/08486756A
; Patent No. 5981711
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/260,190
APPLICATION: UNMBER: US 08/260,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                 TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: U7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8200 GCCTGGCCAACATGGTGAAAACCCCTGTCTCCACTAAAAATACAAAAA 8245
                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
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                                                                                                                                        REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCAC-AAGGTCAGGAGTTTGAGAGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 0.4%;
Local Similarity 86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                    STRANDEDNESS:
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ropology:
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                                   nucleic acid
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DNA (genomic)

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; MOLECULE TYPE:
; HYPOTHETICAL: N
; ANTI-SENSE: NO
US-08-486-756A-65
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                                                                                           US-08-485-862B-65
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Query Match
Best Local Similarity 86.8
Matches 92; Conservative
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Best Local Similarity 86.8%;
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                                                                                                                                                                                                                              TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO:
                                                                                                    MOLECULE NO PROSE: NO
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
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                                                                                                                    MOLECULE TYPE: DN
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/477,504
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8140 ATCCCAGCACTTTGGCAGGCTGAGGCGGGCAGATCACTTGAGGTCAGGAGTTTGAGACCA 8199
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CITY: Tiburon
STATE: California
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                                                                                                                                                                                                                                                                                                     NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/485,862B FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                              LENGTH:
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                           86.8%;
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                           Score 72.8; DB 4; Length 105; Pred. No. 1e-06;
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              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
                                                                                                                                                            TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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                MOLECULE TYPE: DN
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0)
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
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ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                            TOPOLOGY:
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                                                                               STRANDEDNESS:
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                                                                                               nucleic acid
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369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pastorek, Jaromir
WENTION: MN Gene and Protein
                                                                                                                                                                               415-981-0332
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07-JUN-1995
                                     DNA (genomic)
                                                                               double
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                                    RESULT 12
US-08-340-426D-91
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Patent No.
 Sequence 91, Application US/08340426D Patent No. 5948634
                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 371-260
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                                                                                                        12959 AAAGTGCTGGGATTACAGGCATG 12981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwid, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE DOCKET NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                      Local 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCAC--AAGGTCAGGAGTTTGAGAGCA 48
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                                                                                                         61 AAAGTGCTGGGATTACAAGCGTG
                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
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                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 84 base pairs
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                                                                                                                                                                                                                                                               Similarity
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Pred. No. 1e-06;
0; Mismatches 12;
                                                                                                                                                                                                                                                             Score 63.8; DB 3; Pred. No. 6.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0609.3840003
                                                                                                         83
                                                                                                                                                                                                                                               Mismatches
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Best Local Similarity 85.5%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                          Sequence 91, Application US/08450673C Patent No. 5948888 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12959 AAAGTGCTGGGATTACAGGCATG 12981
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
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LENGTH: 84 base pairs
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Neural Thread Protein Gene Expression TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                     APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                               STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                       COUNTRY: U.S.A. ZIP: 20005-3934
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TOPOLOGY: both
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SOFTWARE:
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1100 New York Avenue, Suite 600
                                                                                                                                                                                         E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
PatentIn Release #1.0,
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Pred. No. 6.8e-05;
n: Mismatches 12;
Version #1.25
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/01 FILING DATE: 30-MAY-1995

US/08/450,673C

CLASSIFICATION:

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Best Local Similarity 85.5%;
Matches 71; Conservative
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12899 CCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCGGCCTCGGCCTCCC 12958
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                                                       NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36.203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Ludwig, Steven R.
                                                                                                                                                                               APPLICATION NUMBER: 08/34
FILING DATE: 14-007-194
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                  LENGTH:
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nucleic acid
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                  84 base pairs
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Pred. No. 6.8e-05;
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RESULT 15
US-08-454-557C-70
; Sequence 70, Applicatio
; Patent No. 5830670
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION 1756600
                                                                                                                                                          Query Match 0.3%;
Best Local Similarity 85.9%;
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Best Local Similarity
                                                                                                                                             Matches
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                                                                                                       13556 ACCATGCCTGGGTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGACCAGG 13615
                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                 13616 CTGGTCTCAAACTCCTGA 13633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New 1 CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
61
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                         78 base pairs
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                                                                                                                                                          Score 60.4; DB 3;
Pred. No. 0.00034;
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Search completed: June 17, 2000, 10:50:33 Job time: 251763 sec

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0% Listing first 45 summaries
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GenEmbl:*
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(without alignments)
-1568.842 Million cell updates/sec
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22034
1 TTCGGAGTGATTTTGGTCAT.....TGTGTGTGTGTGTGTGTGTGTG 22034
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_inl:*
gb_in2:*
gb_in2:*
em_ba2:*
em_ba2:*
em_hum3:*
em_hum4:*
gb_pr4:*
gb_htg3:*
gb_htg5:*
gb_htg5:*
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em_sy:*
em_un:*
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em_or:*
em_ov:*
em_pat:*
em_ph:*
em_pl:*
em_ro:*
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em_hum1: *
em_hum2: *
em_in: *
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gb_pr3:*
gb_sts:*
gb_sy:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 (bases 1 to 107)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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                                                                                                                                                                                                                                                                                   Homo sapiens
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1 (bases 1 to 108)
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               /tissue_type="carcinoma"
30 c 35 g 14
                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
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Pred. No. 3.2e-06;
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franscripts
J. Mol. Bio
                         Eutheria; Primates; Catarrhini;
1 (bases 1 to 108)
Shaikh, T.H., Roy, A.M., Kim, J., I
CDNAs derived from primary and s
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Data kindly reviewed (07-DEC-1987)
Location/Qualifiers
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                                                                                    Eukaryota; Metazoa;
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1 (bases 1 to 108)
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/db_xref="taxon:9606"
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Pred. No. 4.9e-05;
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Pred. No. 5.6e-05;
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                           small cytoplasmic Alu
                                             Batzer, M.A. and Deininger, P.L.
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2 (bases
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES 5.
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Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences i the low-density-lipoprotein-receptor gene. A possible mechanism the defect in a patient with familial hypercholesterolaemia the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Shaikh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
 l Similarity
95; Conserv
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes
1. .108
                                                                                                /note-"deletion junction region intron 40 \text{ c} 20 \text{ g} 28 \text{ t}
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39 c 30 q
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/db_xref="taxon:9606"
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Pred. No. 0.00014;
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See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion occurred between
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading fram
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
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1 (bases 1 to 108)
                                                                                                                                         Human carcinoma
M87896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES
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Pred. No. 0.00014;
0; Mismatches 12;
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14 deletion junction.
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RESULT 9
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 Human LDL-receptor
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 104)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
                   HSLDLRD1
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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26 c 37 g 19
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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27 c 33 g 1
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/sex="male"
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See XO5248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion occurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
                                              *source: hypercholesterol aemia
See XJ0250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion occurred between to
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
                                                                                                                                                      Horsthemke,B., Beisiegel,U., Dunning,A., Havinga,J.R., Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
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              of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shaikh, T.H., Roy, A.M., Kim, J., cDNAs derived from primary and
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Human small cytoplasmic
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1 (bases 1 to 108)
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/rpt_type=dispersed
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/db_xref="taxon:9606"
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Local Similarity 86.3%;
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1 (bases 1 to 107)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D. Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. (1992) In press
Location/Qualifiers

1. .107
 l Similarity
86; Conserv
                                                                                                                                                                                                                         Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
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Alu repeat.
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ilarity 87.8%;
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/cell_line="NTera2D1"
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30 c 35 g 1
                                                                                                                     /dev_stage="embryo"
/sex="male"
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/db_xref="taxon:9606"
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                                                                  Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences i the low-density-lipoprotein-receptor gene. A possible mechanism the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
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Human LDL-receptor g
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Human carcinoma cell-derived Alu RNA transcript, clone CE43.
               see X05249 for deletion junction Data kindly reviewed (07-DEC-1987)
                                                                                                                                                                                                                                             Homo sapiens
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/sex="male"
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/db_xref="taxon:9606"
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14751 CTCAAGTGATCCACAATCCTTGGCCTCCCAAA 14782

TTCAAGTGATCCGTCTGCCTTGGCCTCCCAAA 92

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Query Match 0.3%; Score 67.6; DB 1; Length 108; Best Local Similarity 82.6%; Pred. No. 0.065; Matches 76; Conservative 1; Mismatches 15; Indels

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XRESULT PPR DDT CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	000 000 0
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X12095 standard; DNA; 108 BP. X12095; X12095; 30-MAR-1999 (first entry) Human blallelic polymorphic DNA fray Polymorphism; bhallelic; human; fora detection; phenotypic typing; charaa autoimmune disease; cancer; inflamm treatment; marker; ss. MO9820105-A2. 14-MAY-1998. 15-NOV-1997; U20313. 05-NOV-1997; U20313. 06-NOV-1996; US-030455. (WHED) WHITENEAD INST BIOMEDICAL RI Hudson T, Lander ES, Wang D; WPI; 98-286974/25. Wew isolated nucleic acid segments : determining polymorphic forms for u: testing or phenotypic typing for di: Claim 1: Page 219; 310pp; English. X10269-X12937 are human DNA fragment x10269-X12937 are human DNA fragment in the appropriate IUPAC-IUB ambiguity methods for determining polymorphic e.g. forensics, paternity testing o: such as agammaglobulinemia, diabettes muscular dystrophy, Wiskott-Aldrich hypercholesterolemia, polycystic kis spherocytosis, von Willebrand's diss haemorrhagic telangiectasia, familia spherocytosis, von Willebrand's diss haemorrhagic telangiectasia, familia spherocytosis, von Willebrand's diss haemorrhagic telangiectasia, familia syndrome, osteogenesis imperfecta, a autoimmune diseases, inflammation, system, infection by pathogenic mic; as longevity, appearance (e.g. bald endurance, fertility, and susceptib- drugs or therapeutic treatments. The segments can also be used to produc prophylaxis of such diseases. 23 C. Sequence 108 BP; 19 A; 23 C.	444 448 447 477 477 478 478
standard; DNA; 108 BP. Si, biallelic polymorphic DNA Diallelic polymorphic DNA Diallelic polymorphic DNA Diallelic; human; DNA DISS-A2. V-1997; U20313. V-1997; U20313. V-1997; U20313. V-1997; U30313. V-1996; U3-030455.) WHITEREAD INST BIOMEDIC AT, Lander ES, Wang D; BS-286974/25. BS-286974/26. BS-286974	00000000000
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Characteristics of the comprises one of the 7837 "GS" sequences

Cyliven in T19001-T26837 and which is able to hybridise to part of

Chuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

CC sequences were obtained from 3'-directed cDNA libraries prepared

CC from various human tissues; synthesis of cDNA was initiated from the

CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

CC untranslated sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

CC is constructed so as to reflect accurately the relative abundance of

CC different mRNAs in the particular tissue from which it was derived.

CC determined (esp. using primers and probes derived from the GS

CC sequences) as a means of diagnosing abnormal cell function or for

CC crecognising different cell types.

SQ sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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Best Local
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                                                                                                                                                                                                                                                                                human; Cloning, marracell typing; abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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W09514772-A1.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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WPI; 95-2069
                                                                                                                                                                                                                                             Homo sapiens.
WO9514772-A1.
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Identifying
                                                  (OKUB/) OKUBO K.
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                                                                                                                     MATS/) MATSUBARA K.
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gene signatures in 3'-directed human cDNA library -
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78.8%;
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Claim 2; A single-stranded DNA) which comprises one of the 7837 "GS" sequences

Claim 1; Page 1748; Comprises one of the 7837 "GS" sequences

Claim 1; Page 1748; Carleton 2; 
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Best Local
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WPI; 95-20
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Sequence 108 BP; 18 A; 33 C; 23 G; 28 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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l2-NOV-1993; JP-355504.
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Pred. No.
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RESULT 6
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                                                                                                                                                                                                                          11843 GCAACCTCCGCCTCCCGGGTTCAAGTGAT 11871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 91 BP; 18 A; 22 C; 28 G; 18 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection;
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l2-NOV-1993; JP-355504
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Sequence 108 BP; 34 A; 31 C; 26 G; 15 T;
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Best Local S
Matches 78
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W09514772-A1.

01-JUN-1995.

11-NOV-1994; J01916.

12-NOV-1993; JP-355504.
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Gene signature; messenger RNA; mRNA; relative abundance.
human; cloning; mapping; non-blased library; diagnosis;
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05-NOV-1996 (first entry)
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WPI; 95-206931/27
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07-NOV-1996 (first entry)
                                                Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that
                                                                                                            Matsubara K, Okubo
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                             cell typing; abnormal cell function; ss.
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12-NOV-1993; JP-355504.
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                                                                                                                                                                                                 (MATS/) MATSUBARA K.
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                           abundance
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Pred. No. 0.44
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RESULT
T26213
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SQ Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
        δÃ
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double-stranded DNA) which comprises one of the 7837 "GS" sequences

given in T19001-T26337 and which is able to hybridise to part of

thuman genomic DNA, CDNA or mRNA is claimed The GS (Gene Signature)

Sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of CDNA was initiated from the

3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

cuntranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

determined (esp. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for

recognising different cell types.

Sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 74; Conser
                                                                                                                                                                                                                                                                                                     Claim 1; Page 2029; 2245pp; Japanese. A single-stranded DNA (or its complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell typing; abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene signature; messenger RNA; mRNA; human; cloning; mapping; non-biased l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5104 CCTGGGCGACAGAGTAAGACTCCGTTTCAAAAAACAAAAA 5142
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                                                                                                                                                                                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                              tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsubara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T26213 standard;
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12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OKUB/) OKUBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laim 1; Page 1720;
single-stranded DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene signature HUMGS08452.
                                                                                                                                                                                                                                                                                                                                                                                                                      Okubo K;
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Pred. No. 0.61
0; Mismatches
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library; diagnosis; detection;
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the 7837 "GS" sequences
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Claim 1; Page 2158; 2245pp; Japanese.

Claim 2; Page 2158; 2245pp; Japanese.

Claim 1; Page 2158; 2245pp; Japanese.

Claim 1; Page 2158; 2245pp; Japanese.

Claim 1; Page 2158; 2245pp; Japanese.

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

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Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 2158; Page 2158; Page 2158; Page 2158;

Claim 2; Page 21
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BACID
                                                                                T26213/c
                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 68
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Best Local S
Matches 75
                                                                                                                                                                                                                                                                               12004 GATCTACCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAG 12063
                                                                                                                                                                                               12064 CCCTGCTTGTCTTTTTATTATA 12087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsubara
WPI; 95-20
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                 T26213 standard; cDNA to mRNA; T26213; 13-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reflects relative abundance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MATS/) MATSUBARA K.
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                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 68; Conserv
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                                                                                                                                                                      NCTGTACTAAGTCTTTTTTTTTA
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Pred. No. 0.91
0; Mismatches
                                                                                                                                                                                                                                                                                                                                           0;
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Human gene signature HUMGS08452

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Best Local S
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                                                                                                01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                         cell typing; abnormal Homo sapiens. W09514772-A1.
                                      Identifying gene signatures in for diagnosis of abnormal cell reflects relative abundance of
                                                                                                                                                                       Gene signature; messenger RNA; mRNA; human; cloning; mapping; non-biased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
            Claim 1; Page 758-759;
A single-stranded DNA (
                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-1994; J01916.
12-NOV-1993; JP-355504
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; cloning; mapping; non-biased cell typing; abnormal cell function;
                                                                       WPI; 95-206931/27
                                                                                 Matsubara K,
                                                                                         (окив/) окиво к.
                                                                                                                                                                                                                          T20927 standard;
                                                                                                                                                                                                                                                                                                                     102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 95-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                              TTTTTTTTTTTTAGACAGAGTCTTACTCTGTCGCCCGGGCTGGAGTGCAGTGGCTCGA 10318
                                                                                                                                                                                                                                                                                               TCTTAGCTCACTGAAAGCTTTGCCTCCCGGGTTCATGCCAT 10359
                                                                                                                                                                                                                                                                           TCATAGCTCACTGTAACACCCAAACTCCTGGACTCAAGTGAT 2
                                                                                                                                                                                                                                                                                                                   TTTTTTTTTTTTAAAGACATGTTCTTACTCTGTGGCCCCAGGCTGGAGTGCAGTGGTGCCA 43
                                                                                                                                                                                             gene signature HUMGS02180.
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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   DNA)
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99; 2245pp; Japanese.
WA (or its complementary strand or the which comprises one of the 7837 "GS"
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                                                                                                                                                                cell function;
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                                                                                                                                                                                                                          mRNA;
                                                                                                                                                                                                                                                                                                                                                          ; Score 59.4; pred. No. 0. 0. Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Japanese.
                                               3'-directed human cDNA library -
function, by preparing cDNA that
                                                                                                                                                                                    mRNA;
                                                                                                                                                                                                                          103
                                         corresp.
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                         library;
                                                                                                                                                                SS.
                                                                                                                                                                        relative abundance; frequency;
library; diagnosis; detection;
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                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                    DB
. 97;
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                                        specific
                                                                                                                                                                                                                                                                                                                                                                              Length
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                                         human
         corresp
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RESULT 1
T20373/c
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Claim 1; Page 623; 2245pp; Japanese.
Comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of the 7837 "GS" sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-directed sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
Sequence 107 BP; 26 A; 29 C; 17 G; 29 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     given in T19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                            W09514772-A1.
01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18364
                                                                                                                                                                                                                                                                                                                                                 Identifying gene signatures in for diagnosis of abnormal cell reflects relative abundance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene signature HUMGS01525.
Gene signature; messenger RNA; mRNA; relative
human; cloning; mapping; non-biased library;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                        Matsubara K, Okub
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                             tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T20373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T20373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCCTCCCACTTCCACCTCCCAAGTAGCTGTGGCTACAGGTGTGTGCCACCATGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              Okubo K;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.5
); Mismatches
                                                                                                                                                                                                                                                                                                                                             3'-directed human cDNA library - function, by preparing cDNA that corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              relative abundance; frequency;
library; diagnosis; detection;
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1.5;
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Query Match Best Local S Matches 69

69; Conser

0.3%;

Score Pred.

56.4; No. 2

.6;

1;

Length 107; Indels

0;

Gaps

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RESULT 14

T21566/C

ID 1721566 standard; cDNA to mRNA; 8:
AC T21566;
DT 03-AUG-1996 (first entry)
DE Human gene signature HUMGS02944.
KW Gene signature; messenger RNA; ml
KW human; cloning; mapping; non-bias
KW cell typing; abnormal cell funct:
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2182; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4877
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                                                                                                                                                                                                                                                                                    3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo sapiens.
 Human gene signature HUMGSO2944.

Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                  4911 CATGAGGTCAGGA 4923
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          recognising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene signature HUMGS09078.
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95-206931/27.
                                                                                                                                                                                                GACGAGGTCAGGA 5
                                                                                                                                                                                                                                                                     GCCGGGCGTGGTGGCTCATGCCTGTAANCCCAGCACTATGGGAGGCCGANACGGGCGGAT 18
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                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           different cell types.
108 BP; 18 A; 33 C;
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.4;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                      Score 56.6;
Pred. No. 2
                                                                                                           87
                                                                                                           ₽P
                                      relative abundance;
                                                                                                                                                                                                                                                                                                                                                      2.4;
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                                                                                                                                                                                                                                                                                                                                                                    Length 108;
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                    detection
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T22572
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Best Local
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Claim 1; Page 914; 2245pp; Japanese.

A single-stranded DNA) (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a CDNA library can be determined from the GS.
                                                                                                                                                                                                                                                  01-JUN-1995.
11-NOV-1994;
12-NOV-1993;
Claim 1; Page 1159; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared
                                                                                                                                                                                                                                                                                                   Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo sapiens.

W0951772-Al.
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Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA the
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11-NOV-1994; J01916.
12-NOV-1993; JP-355
                                                                                                                                                                              Matsubara K, Okubo K; WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or recognising different cell types. Sequence 87 BP; 35 A; 21 C; 16 G; 13 T;
                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                             Human gene signature HUMGS04188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
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W09514772-A1.
                                                                                                             tissues
                                                                                                                                                                                                                 (OKUB/) OKUBO K.
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65; Conser
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JP-355504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA to mRNA;
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Pred. No. 4
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from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-tuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 93 BP; 22 A; 23 C; 24 G; 22 T;
                                                                                                                                                                                                                                                      5104 CCTGGGCGACAGAGTAAGACTCCGTTTCAAAA 5135
                                                                                                                                62 CNTTGGTTATNATGCAAGACCCTGTTTACAAA 93
2000, 18:05:14
                                                                                                                                                                                                                                                                                                                                                                                   Score 54.8; DB 1; Length 93; Pred. No. 4.4; 0; Mismatches 24; Indels
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

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(CE 1 (bases 1 to 106)

RS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson, WashU-NCI human EST Project

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On Sep 12, 1996 +hi--
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AA218889 ZQ15d04.s
AA8288124 Od71a07.s
AQ028426 CIT HSP-2
AA24245 DC07a04.s
AA24245 DC07a04.s
AA226556 HC19f09.s
AA02862107 RPC111-94
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AQ240182 CIT-HSP-2
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                   Tan, F.,
Wilson, R.
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Washington University Schoc
4444 Forest Park Parkway, E
Tel: 314 286 1800
Fax: 314 286 1810
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AA243009.
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On Dec 3, 1996 this sequence
Contact: Wilson RK
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1 (bases 1 to 109)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham
                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. i
Tel: 314 286 1810
Fax: 314 286 1810
                    This clone is available royalty-free IMAGE Consortium (info@image.lin1.gov Insert Length: 1127 Std Error: 0.00 Seq primer: -41ml3 fwd. ET from Amers
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/dev_stage="hNT neurons"
/lab_host="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151346
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seq primer: -40ml3 fwd. ET from Amers
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Emmert-Buck, M.D., Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                    www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                        Robert_Strausberg@nih.gov
Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
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/clone="IMAGE:664467"
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                   /clone="IMAGE:1255473"
/clone_lib="NCI_CGAP_GC3"
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                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="pooled germ cell tumors"
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Pred. No. 0.098;
0; Mismatches
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Homo sapiens cDNA clone IMAGE:1255473 3'
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                                                                                                                                                Amersham
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Best Local Similarity 94.1
Matches 96; Conservative
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B65160.1
                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Other GSSs: CIT-HSP-2017G2.TFB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B65160 108 bp DNI
CIT-HSP-2017G2.TRB CIT-HSP
                                                                                                                                                                                                               Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 108)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a random BAC Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
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HindIII"
a 27 c
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                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:7043860"
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                              /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                              Location/Qualifiers
                                                                       /sex="Male"
                                                                                                         /db_xref="taxon:9606"
/clone="2017G2"
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                                                                                        /clone_lib="CIT-HSP"
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                                                                                                                                              99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150764.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This Constraints Television (Ph.D.)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 63.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 834 Std Error: 0.00
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Theritate, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1466067"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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Pred. No. 0.18;
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Best Local Similarity 89.9%;
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                                                                                                                                                                                                                                                                                                                                                  17725 TTTTTTTTTGAGACGGAGTCTCGTTCTGTCACCCAGGCTGGAGTGCAGTGGCACAATCTC 17784
                                                                                                                                                                                                                                                           17785 GGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCTATTCTCCTGCCTCA 17833
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                                                                                                                                                                                                                                               AGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCA 109
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                                                                                                                                                                                                                                                                                                                                                                                      98;
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                                                                                                     genomic survey sequence B65160
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Class: BAC ends.
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Tel: 301 838 0200
Fax: 301 838 0208
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Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
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CIT-HSP-2313G15.TF CIT-HSP
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                              Homo sapiens
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
a 36 c 25 g 29 t
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/clone="2313G15"
                                                                                     GI:2639138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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one 2313G15
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JOURNAL
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Best Local Similarity
Matches 97; Conserv
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                                                                                                                                                                               AUTHORS
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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:636191.
Contact: Wilson RK Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                           AA835205 101 bp
ak64h01.s1 Barstead r
IMAGE:1412689 3' simi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq_primer: M13 Reverse
Class: BAC ends.
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Clones are available from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Other_GSSs: CIT-HSP-2017G2.TFB
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1 (bases 1 to 101)
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/db_xref="GDB:7043860"
/db_xref="taxon:9606"
/clone="2017G2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Sperm"
/note="Yector: pBeloBAC11; Site_1: HindIII; Site_2:
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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nc07a04.s1 NCI_CGAP_Pr1
similar to contains Alu
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                                                                                                                                                                                                                                  Unpublished (1997)
On Jan 24, 1995 this sequence version replaced g1:634306
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AA244245.1
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Seq primer: -41ml3 fwd.
                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy
                                        www-bio.llnl.gov/bbrp/image/image.html
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Similarity 93.1%;
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36 c 27 g 24 t
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with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
ist strand cDNA was primed with a Not I - oligo(dT) primer
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/db_xref="taxon:9606"
/clone="IMAGE:1412689"
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/lab_host="DH10B"
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ET from Amersham
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FEATURES

High quality sequence stop: Location/Qualifiers

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REFERENCE
AUTHORS
TITLE
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KEYWORDS
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                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGAGATTCTTCTGCCTCA 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA228795 103 bp mRNA EST 20-AU3 177, nc14e07.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008132 similar to contains Alu repetitive element;contains element MER28 repetitive element; mRNA sequence.
                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lenion, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On Sep 12, 1996 this sequence version replaced g1:1394473
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                   High quality sequence stop: 81.
Location/Qualifiers
                                                                                                                          Seq primer: -41m13 fwd. ET from Amersham
                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Primates;
1 (bases 1 to 103)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Similarity 88.2%;
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/db_xref="taxon:9606"
/clone="IMAGE:1007406"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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Primates; Catarrhini; Hominidae; Homo.
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RESULT 11
AQ264176/c
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ORGANISM
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Best Local
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                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94;
                                                                                                                                                                                                                                           Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ264176 106 bp DNA CITBI-E1-2509A2.TF CITBI-E1 Homo
                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other_GSSs: CITBI-E1-2509A2.TR
                                                                                                             Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                           end search
                                                                                                                                                                                                  Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                         Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                       Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with Oilgo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                    1. .106
/db_xref="taxon:9606"
/clone="2509A2"
                                         /organism="Homo sapiens"
                                                                                       Location/Qualifiers
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/sex="male"

cell_type="sperm"

/clone_lib="CITBI-E1"

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RESULT 12
B48914/c
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JOURNAL
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Best Local Similarity
10431 TTTTTAGTAGAGACGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCG 10490
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                                                                      Local
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Use of BAC End Sequences for Sequence-Ready Map Building Unpublished (197)
                                                                                                                                                                                                                                                                                                                                                                                                              Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or figesearch Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B48914 103 bp DNA RPCI11-4A12.TP RPCI-11 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
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                                                                                                                                                    /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
a 28 c 30 g 15 t
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                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:7501163"
/db_xref="taxon:9606"
/clone="RPCI-11-4A12"
                                                                                                                                                                                                                           /sex="Male"
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11812 CTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAACCTCCGGCTCCCGGGTTCAAGTGAT 11871
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                                                         CTGGAGTGCAGTGGCTCAATCTCAGCTCACTGCAAGCTCTGCCTCCCAGGTTCAAGTGAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On Sep 12, 1996 this sequence version replaced g1:1393355
Contact: Robert Strausberg, Ph.D.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Cancer Genome Anatomy
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                Conservative
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                                                                                                                                                                                           Location/Qualifiers
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Homo sapiens cDNA clone IMAGE:1016157 3'
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RESULT 14 AQ535244/c

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Matches 92; Conservative
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 Zhao,
                                                                                                                                                                                   AQ582186 103 bp DNA
RPCI-11-451A15.TJ RPCI-11 Homo
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               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 103)
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Use of BAC End Sequences
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Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
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/note="Vector: pBACe3.6; Site_1:
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a 27 c 27 g 18 t
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/db_xref="GDB:7621533"
/db_xref="taxon:9606"
/clone="RPCI-11-317H22"
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (lnfo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg_primer: SP6
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Venter, J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready

Map Bullding

Unpublished (1997)

On Feb 19, 1999 this sequence version replaced gi:4146076.

Other_GSSs: RPCI-11-451A15.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Tel: 301 838 0208

Fmail: hheatter Dr.
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                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI;
/RPCI11 Human Male BAC Library"
a 36 c 25 g 22 t 1 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
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/db_xref="taxon:9606"
/clone="RPCI-11-451A15"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                        0.4%;
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Sequence

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Post-processing:
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length: 110
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Listing first 45
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US-08-787-739-65
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US-08-440-4260-91
US-08-440-4260-91
US-08-440-4260-91
US-08-440-673C-91
US-08-454-57C-70
US-08-454-57C-70
US-08-454-57C-70
US-08-454-657C-92
US-08-450-673C-92
US-08-485-655
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Compugen Ltd
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  Sequence
                                                                                                                                                                                                                                                                                             Description
  MOLECULE TYPE: I
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-481-658B-65
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US-08-481-6588-65
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GENERAL INFORMATION:
                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
Query Match
Best Local Similarity
                                                                                                                                            APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-435-2034
TELEPAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                               ZIP: 94920
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                                                                      DNA (genomic)
  0.3%;
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US-08-340-426D-69
US-08-450-673C-69
US-08-454-557C-57
US-08-450-673C-57
US-08-450-673C-57
US-08-450-673C-71
PCT-US95-17111A-57
US-08-750-064-6
US-08-750-064-6
US-08-340-426D-60
US-08-450-673C-60
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US-08-450-673C-65
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US-08-450-673C-65
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No. 5.6e-07;
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Result No.

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Length 105

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Minimum DB Maximum DB

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Best Local Similarity
Watches 87; Conserve
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RESULT
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
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                                                                                                  GENERAL INFORMATION:
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                                                                       10482 CTGACCTCGTGATCCGCCCACCTGAGCCTCCCAAAGTGCTGGGAT 10526
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IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/08/477,504^A
CLASSIFT***
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APPLICANT:
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                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION UNDER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MN Gene and Protein NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                           61
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STATE: Califor
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                            Score 76.2; DB 4; Length 105; Pred. No. 5.6e-07; 0; Mismatches 18; Indels
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Patent No. 5981711
                                                                                                                                                  Sequence 65, Application US/08485862B Patent No. 5989838
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Best Local Similarity
                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                              APPLICANT: Zavada, Jan
APPLICANT: Pastorekova,
APPLICANT: Pastorek, Jar
TITLE OF INVENTION: MN G
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                     10422 TTTTTGTATTTTTTAGTAGAGACGGGGTTTCACCCATGTTAGCCAGGATGGTCTCGATCTC 10481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: D-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-0727
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FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: Leona L.
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUN-
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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STREET:
                 ADDRESSEE:
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6 Mariposa Court
                                  Pastorek, Jaromii
VENTION: MN Gene and Protein
PROMENCES: 86
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                 Leona L.
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Pred. No. 5.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
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ZIP: 94920 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: USA

California

94920

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FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY,AGENT INFORMATION:
NAME: Lauder Leona L.
REGISTRATION NUMBER: 0-0021.3D
REFERENCE/DOCKET MUMBER: 0-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                 Patent No. 6027887
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        Sequence 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10482 CTGACCTCGTGATCCGCCCACCTGAGCCTCCCAAAGTGCTGGGAT 10526
                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DN
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                       APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CTGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
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                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                               94104
                                                                                                                                                                                                                                                                                                                                                      5, Application US/08787739
6027887
                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                     Zavada, Jan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.3%; Score 76.2; DB 4; Length 105; 82.9%; Pred. No. 5.6e-07;
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                                                                                                                                                                                                                                                 Sequence 91, Application US/08454557C Patent No. 5830670
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Best Local Similarity
Matches 87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lauder, Leona L.
REGISTION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
                                                                                                                                                 APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/485,863 FILING DATE: 07-JUN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/487,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/485,862 FILING DATE: 07-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUN-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                    STREET: 1100 New CITY: Washington STATE: D.C.
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                             COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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                  20005-3934
                                                  D.C.
                                                                                     E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
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24-JAN-1997
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82.9%;
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Pred. No. 5.6e-07;
0; Mismatches 18
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                                                                                                                                                                           Expression and Detection
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NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE_DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:

0609.3840003

LENGTH:

ATTORNEY/AGENT INFORMATION:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514

MEDIUM TYPE: COMPUTER: II

IBM PC compatible Floppy disk

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US-08-454-557C-91
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Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 91,
                                               CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAAGTGCTGGGATTACAAGCGTG
                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                           E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                              Release #1.0, Version #1.25
                                                                                                                                                                                           US/08/340,426D
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                                                                                      0609.3840002
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Pred. No. 3.6e-05;
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10514 AAAGTGCTGGGATTACAGGTGTG 10536

AAAGTGCTGGGATTACAAGCGTG

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QY 10454 CCATGTTAGCCAGGATGGTCTCGGATCTCCTGAGCTCGGTGATCCGGCCCACCTGAGCCTTCCC 10513
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                                                                                                                                                                                                                                                                                US-08-450-673C-91
                                                  Query Match
Best Local Similarity 85..
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 91, Patent No. 5
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Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                nucleic acid
DEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                    84 base pairs
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                                                                                                Score 67; DB 4; Pred. No. 3.6e-05; No. 3.6e-05; No. 3.6e-05; No. 3.6e-05; No. 200; N
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Pred. No. 3.
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                                                                                                                                                                        Length 84;
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US-08-454-557C-91/c
Sequence 91, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
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PCT-US95-17111A-91
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Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                               10514 AAAGTGCTGGGATTACAGGTGTG 10536
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NFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/340,426
                                                                        TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/34 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                       CORRESPONDENCE ADDRESS:
                                                                                                                           APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R
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APPLICANT: Wands, Jack R.
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                    STREET:
                                                                                                                                                                                                                                                                                               61 AAAGTGCTGGGATTACAAGCGTG 83
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STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                     1 CCATGTTCATCAGGCTGTGTCGAACTCCTGACCTCGTGATCCGCCCCCCCTCAGCCTCCC 60
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Washington
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                   1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 base pairs
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Detection of Alzheimer's Disease
121
                                    Kessler, Goldstein & Fox P.L.L.C
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Pred. No. 3.6e-05;
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Best Local Similarity 83.1%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                       SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
               REGISTRATION NUMBER: 36,200
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION
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MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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APPLICANT: Wands, Jack R.
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
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                                                                                                                                                                                                                                                                                                                 STREET: 1100 New CITY: Washington STATE: D.C.
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TELEPHONE:
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20005-3934
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                                    0609.3840002
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Pred. No. 0.0007;
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                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity 83.1%;
                                                                                               Matches
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                                                                                                                                                                                                                                                                            TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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 4927 CAAGACCAGCCTGACCAATATGG 4949
                                                            SEQUENCE CHARACTERISTICS:
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                                 83
                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                               TOPOLOGY: bo
                                                                                                                                                                                                                                                                                                                                                    NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
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                              69;
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                                                                                                                                                                                                                                          84 base pairs
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                                                                                               Conservative
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                                                                                          0.3%; Score 60.6; DB 4; Length 84; 83.1%; Pred. No. 0.0007; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/450,673C
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                                                                                                                                                                                                                                                                                                                                             0609.3840004
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                                                                                             0;
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US-08-454-557C-70

; Sequence 70, Application US/08454557C

; Patent No. 5830670
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; Sequence 91, Application PC/TUS9517111A

; GENERAL INFORMATION:
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Best Local Similarity 83.1%;
                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                           APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                               4927 CAAGACCAGCCTGACCAATATGG 4949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ludwig, Steven R.
REGISTON NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/:
FILING DATE: 14-NOV-199
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expre:
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                NUMBER OF SEQUENCES: 1
                                                      TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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  ADDRESSEE:
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)EDNESS: both
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Sterne, Kessler, Goldstein & Fox P.L.L.C
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STREET: 1100 New CITY: Washington STATE: D.C.

1100 New York Avenue, Suite 600

COUNTRY: U.S.A. ZIP: 20005-3934

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36.203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base 12456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 70, Application Patent No. 5948634
GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                  ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,
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MEDIUM TYPE: Floppy disk
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                       APPLICATION NUMBER: US/08/340,426D FILING DATE: 14-NOV-1994 CLASSIFICATION: 435
REFERENCE/DOCKET NUMBER: 060
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08340426D
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; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-340-426D-70
Search completed: June 17, 2000, 17:39:10 Job time: 276280 sec
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                                                                                                                                                                                 Matches
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Best Local Similarity 84.6%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
                                                                                                14732 CTGGTCTCGAACTCCTGA 14749
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 371-2600
                                                                     61 CTGGTGTCGAACTCCTGA 78
                                                                                                                                                                                  66;
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Pred. No. 0.0016;
0; Mismatches 1
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